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GenCore version 5.1.6
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Scoring table:

⁹⁴¹⁶⁴⁶⁶ Total number of hits satisfying chosen parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AB034967 Bos tauru	AB040058 Ovis arie	AB040059 Bos tauru	AB040060 Bos tauru	AB040061 Bos tauru	AB034981 Bos tauru	M18780 Bovine alph	X06367 Ovine mRNA	J05147 Bovine alph	AB052168 Ovis arie	AB052163 Bos tauru	AB052164 Bos tauru	AB052166 Bos tauru	AB052167 Bos tauru	AB052165 Bos tauru	M90645 Cow alpha-l	AR066426 Sequence	AF194373 Bubalus a	AF194372 Bos grunn
	ID	AB034967	AB040058	AB040059	AB040060	AB040061	AB034981	BOVLACTBA	OALACA	BOVALACT	AB052168	AB052163	AB052164	AB052166	AB052167	AB052165	BOVLACTALB	AR066426	AF194373	AF194372
	DB	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	9	4	4
	Query Match Length DB	283	283	283	283	283	295	703	723	724	1855	1868	1870	1870	1871	1896	2044	2044	2784	2999
de	Query Match	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1
	Score	58	58	58	58	58	28	28	58	58	28	28	28	28	28	28	28	58	58	28
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	AY726609 Bubalus b		AY/Zeell Bubalus D	AND ADDA SELECT	XA6366 Boyine gene		AR452811 Seguence	AX359937 Seguence	AX382151 Seguence	AY726612 Bubalus b	AX359930 Seguence	AX382144 Sequence	AX359931 Sequence	AX382145 Sequence	AX359932 Seguence	AX382146 Sequence	AX359933 Sequence	AX382147 Sequence	AX359929 Sequence	AX382143 Sequence	AX359934 Sequence	AX382148 Sequence	AX359939 Sequence	AX382153 Sequence
AC150961	AY/26609S1	AI/Zeelusi	AY /26611S1	AE240906	RT1,ACTA	GOTALAL	AR452811	AX359937	AX382151	AY726612S1	AX359930	AX382144	AX359931	AX382145	AX359932	AX382146	AX359933	AX382147	AX359929	AX382143	AX359934	AX382148	AX359939	AX382153
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ALIGNMENTS

⁴⁷⁰⁸²³³ seqs, 24227607955 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

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Submitted (13-MR-2000) Nacyuki Yamamoto, National Agricultural
Research Organization, National Agricultural Research Center for
Hokkaido Region, Laboratory of Animal Breeding and Genetics; 1
Hitsuljaga
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Yamamoto, N. and Moritsu, Y.
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Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                          /mol type="genomic DNA"
/strain="Angus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="blood"
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95. .283
                                                                                           Yamamoto, N. and Moritsu, Y.
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/gene="a-LACTA"
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Eukaryota, Metazoa,
Mammalia, Eutheria,
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AB040060
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CEFPAILLCPIIHPLHSFP"
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Submitted (13-MR-2000) Nacyuki Yamamoto, National Agricultural Research Organization, National Agricultural Research Organization, National Agricultural Research Organization, Laboratory of Animal Breeding and Genetics; 1 Hitsuljigaokka, Toychira, Sapporo, Hokkaido 062-8555, Japan (E-mail:nymmt@affrc.go.jp, Tel:81-11-857-9270, Fax:81-11-859-2178)
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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Bos taurus a-LACTA gene for alpha-lactalbumin, partial cds,
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                                   92.1%; Score 58; DB 4; Length 283; 100.0%; Pred. No. 2.4e-10; ive 0; Mismatches 0; Indels
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Published Only in Database (2000)
2 (bases 1 to 283)
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larity 100.0%; Pred. No. 2.4e-10;
Conservative 0; Mismatches. 0;
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a-LACTA; alpha-lactalbumin.
Ovis aries (sheep)
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a-LACTA; alpha-lactalbumin.
Bos taurus (cow)
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58; Conserva
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                                                                                                                                                                                                                                                                                                                                             MAM 30-MAY-2002
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Submitted (15-NOV-1999) Naoyuki Yamamoto, National Agricultural
Submitted (15-NOV-1999) Naoyuki Yamamoto, National Agricultural Research Center for
Research Organization, National Agricultural Research Center for
Hokkaido Region, Laboratory of Animal Breeding and Genetics; 1
Hitsujigaoka, Toyohira, Sapporo, Hokkaido 062-8555, Japan
(B-mail:nymmt@affrc.go.jp, Tel:81-11-857-9270, Fax:81-11-859-2178)
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                          103 ATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG 160
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                              Length 283;
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Bos taurus gene for alpha lactalbumin, partial cds.
AB034981
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Bovine alpha-lactalbumin mRNA, complete cds:
M18780
                           Query Match 92.1%; Score 58; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 58; Conservative 0; Mismatches 0;
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2 (bases 1 to 295)
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/tissue_lib="blood"
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Bos taurus (cow)
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lactalbumin.
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Bos taurus
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CEFPAILLCPIIHPLHSFP"
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Bos taurus a-LACTA gene for alpha-lactalbumin, partial cds,
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CEFPAILLCPIIHPLHSFP"
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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/db_xref="G1:7288124"
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                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAA92834.1"
/db_xref="GI:7288122"
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/mol_type="genomic DNA"
/strain="Jersey"
                              /mol_type="genomic DNA"
/strain="Hereford"
organism="Bos taurus"
                                                                                 /db_xref="taxon:9913"
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                                                                                                                                    /tissue_type="blood"
/dev_stage="adult"
95. .783
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/dev_stage="adult"
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a-LACTA; alpha-lactalbumin.
Bos taurus (cow)
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95. .>283
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                                                                                                                  /sex="female"
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/db_xref="G1:163283"
/tb_xref="G1:163283"
/translation="MMSFVSLLVGILFHATQAEQLTKCEVFRELKDLKGYGGVSLPBWVCTTFHTSGYDTQATVQNNDSTBYGLFQINNKIWGKDDQNPHSSNICNISCDKFLDDDLTDDIMCVKKILDKVGINYMLAHKALCSEKLDQWLCEKL"
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[ (basea 1 to 723)
[ daye, P., Hue-Delahaie, D., Mercier, J.C., Soulier, S., Vilotte, J.L. and Furet, J.P.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                  Original source text: Bovine (strain Holstein) lactating mammary
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                                                                                                                                                                                  gland, cDNA to mRNA, clone pB-alpha-LA5.
Draft entry and computer-readable form of sequence [1] kindly provided by W.L.Hurley 25-MAR-1988.
Location/Qualifiers
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Biochimie 69 (6-7), 601-608 (1987)
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                        1 (bases I to 703)
Hurley, W.L. and Schuler, L.A.
Molecular cloning and nucleotide sequence of a bovine alpha-lactalbumin cDNA
Gene 61 (1), 119-122 (1987)
                                                                                                                                                                                                                                                                         /mol_type="mRNA"

/ Laref="taxon:9913"

/ Laref="taxon:9913"

/ Laref="alpha-lactalbumin precursor protein"

/ codon_start=1
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    .65
    /note="alpha-lactalbumin signal peptide"

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/clone lib="mammary cDNA"
27. .455
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0; Mismatches
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/product="alpha-lactalbumin"
/protein_id="CAA29665.1"
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upstream of AluI site.
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Ovine mRNA for alpha-lactalbumin.
X06367
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alpha-lactalbumin; lactalbumin.
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               Mammalia, Eut.
Bovinae, Bos.
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58; Conserv
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/db_xref="G1:1310"
/db_xref="G0A:P09462"
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DITDDIVCAKKILDKVGINYMLAHKALCSEKLDQWLCEKL"
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WVCTTFHTSGYDTQAIVQNNDSTEYGLFQINNKIWCKDDQNPHSSNICNISCDKFLDD
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 724)
Wang,M., Scott,W.A., Rao,K.R., Udey,J., Conner,G.E. and Brew,K. Recombinant bovine alpha-lactalbumin obtained by limited proteolysis of a fusion protein expressed at high levels in Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="alpha-lactalbumin signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOVALACT 724 bp mRNA 1
Bovine alpha-lactalbumin mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 264 (35), 21116-21121 (1989) 90078209
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0
                                                                                                                                                                                                                                                                                                                92.1%; Score 58; DB 4; Le ilarity 100.0%; Pred. No. 2.5e-10; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.5e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                /product="alpha-lactalbumin"
705. .710
723
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/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9913"
28, .456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Best Local Similarity luv..
Best Local Si Conservative
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Best Local Similarity
Matches 58; Conserv
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polyA_site
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mat_peptide
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AB052168

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/translation="mmsfyglilvgilfhatqaeqltkcevfrelkdlkgyggvslpe
wvcttfhtsgydtqaivqnndsteyglfqinnkiwckddqnphssnicniscDkfldd
Dltddimcvkkildbkvginywlahkalcsekldqwlcekl"
                  Direct Submission
Submitted (05-DEC-2000) Naoyuki Yamamoto, National Agricultural
Research Organization, National Agricultural Research Center for
Hokkaido Region, Laboratory of Animal Breeding and Genetics; 1
Hitsujigaoka, Toyohira, Sapporo, Hokkaido 062-8555, Japan
(B-mail:nymmt@affrc.go.jp, Tel:81-11-857-9270, Fax:81-11-859-2178)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 ATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG 154
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                                                                                                                                                                                                                                                                                                                                join(97. .229,551. .709,1183. .1258,1763. .1823)
/gene="alacta"
join(97. .229,551. .709,1183. .1258,1763. .1823)
/gene="alacta"
/codon_start=1
/product="alpha lactalbumin"
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join(96. .228,550. .708,1182. .1257,1762. .1822)
/gene="alacta"
join(96. .228,550. .708,1182. .1257,1762. .1822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 1868; 2.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABO52164 linear 1870 bp DNA linear Bos taurus gene for alpha lactalbumin, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              th 92.1%; Score 58; DB Similarity 100.0%; Pred. No. 2.7 58; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB18921.1"
/db_xref="GI:11610589"
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Published Only in Database (2000)
2 (bases 1 to 1870)
                                                                                                                                                                                              /organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Jersey"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="Hereford"
/db_xref="taxon:9913"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus"
                                                                                                                                                                                                                                                                    db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                           /tissue_type="blood"
join(97. .229,551. .
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                                                                                                                                                                                                                                                                                         /sex="female"
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                1. .1868
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Matches 58; Conserv
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    Yamamoto, N.
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                                                                                                                                                         FEATURES
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/db xref="G1:11610599"
/db xref="G1:11610599"
/db xref="G1:11610599"
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WVCTAFFTSGYDTQATUQNNDSTEYGLFQINNKIWCKDDQNFHSRNICNISCDKFLDD
DLTDDIMCVKKILDKVGINYWLAHKALCSEKLDQWLCEKL"
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                                                                   MAM 30-MAY-2002
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Bos taurus gene for alpha lactalbumin, complete cds, strain:Jersey.
ABO52163
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-DEC-2000) Naoyuki Yamamoto, National Agricultural Research Organization, National Agricultural Research Center for Hokkaido Region, Laboratory of Animal Breeding and Genetics; 1 Hitsujigaoka, Toyohira, Sapporo, Hokkaido 062-8555, Japan (E-mail:nymnt@affrc.go.jp, Tel:81-11-857-9270, Fax:81-11-859-2178) i. 1855
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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join(95.227,554..712,1186..1261,1766..1826)
/gene="alacta"
join(95..227,554..712,1186..1261,1766..1826)
/gene="alacta"
                                                Ovis aries gene for alpha lactalbumin, complete cds, strain:Corriedale.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="alpha lactalbumin"
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Published Only in Database (2000)
2 (bases 1 to 1868)
                                                                                                                                                                                                                                                                                                                                                   Ovis aries alpha lactalbumin
Published Only in Database (2000)
2 (bases 1 to 1855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="Corriedale"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Ovis aries"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9940"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB052163.1 GI:11610588
                                                                                                                                                       AB052168.1 GI:11610598
                                                                                                                                                                                                   Ovis aries (sheep)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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AB052163

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Gaps

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MAM 30-MAY-2002

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Bos taurus gene for alpha lactalbumin, complete cds, strain:Angus.
ABO52165
                                      MAM 30-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission

Submitted (05-DEC-2000) Nacyuki Yamamoto, National Agricultural
Research Organization, National Agricultural Research Organization, National Agricultural Research Organization, Laboratory of Animal Breeding and Genetics; 1
Hitsuljigaokka, Toychira, Sapporo, Hokkaido 062-8555, Japan
(E-mail:nymmtGaffrc.go.jp, Tel:81-11-857-9270, Fax:81-11-859-2178)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                    Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae, Bovinae, Bos.
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//gene="alacta".
join(113. .245,567. .725,1199. .1274,1779.
//gene="alacta"
                                    AB052167 1871 bp DNA linear
Bos taurus gene for alpah lactalbumin, complete cds.
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Published Only in Database (2000)
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2 (bases 1 to 1896)
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                                                                                                                         AB052167.1 GI:11610596
                                                                               strain:Japanese black
                                                                                                                                                                  Bos taurus (cow)
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Les 58; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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/gene="alacta"
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Bos taurus gene for alpha lactalbumin, complete cds,
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                                                                                                                                                                                 92.1%; Score 58; DB 4; Length 1870;
100.0%; Pred. No. 2.7e-10;
ive 0; Mismatches 0; Indels
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/trānslation="MMSFVSLLLVGILPHATQAEQLTKCEVFRELKDLKGYGGVSLPE
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DLTDDIMCVKKILDKVGINYWLAHKALCSEKLDQWLCEKL"
Direct Submission
Submission
Submitted (05-DEC-2000) Nacyuki Yamamoto, National Agricultural
Research Organization, National Agricultural Research Center for
Hokkaido Region, Laboratory of Animal Breeding and Genetics; 1
Hitsujigaoka, Toyohira, Sapporo, Hokkaido 062-8555, Japan
(E-mail:nymmt@affrc.go.jp, Tel:81-11-857-9270, Fax:81-11-859-2178)
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                                                                                                                                                                                                                                                                                                                                                                                        / Lear towner type="blood"
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122 ATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG 179 1 ATGATGTCCTTTGTCTCTCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG 58 0; Gaps Query Match 92.1%; Score 58; DB 4; Length 1896; Best Local Similarity 100.0%; Pred. No. 2.7e-10; Matches 58; Conservative 0; Mismatches 0; Indels g ò

Search completed: October 1, 2005, 14:10:02 Job time : 1083.59 secs

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                                                   October 1, 2005, 11:36:51; Search time 372.982 Seconds (without alignments) 999.897 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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5112 5113 5114 5114 5114 5114 5114 5114 5114	27.8 27.8 26.8 26.8
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ALIGNMENTS

New fusion protein comprising the activities of N-acetylgalactosaminyltransferase, lactosyltransferase and glucosyltransferase, useful for producing recombinant glycoproteins. Location/Qualifiers 28. .456 /*tag= b /product= "Bovine alpha-lactalbumin" Alpha-lactalbumin; cattle; glycoprotein; gene; ss. (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG. RESULT 1 ADF18445 ID ADF18445 standard; cDNA; 724 BP. Bovine alpha-lactalbumin cDNA 16-APR-2002; 2002KR-00020544. 16-APR-2003; 2003WO-KR000773 28. .84 /*tag= a 85. .453 /*tag= c (first entry) Lee K, Kang Y; WPI; 2003-854120/79. P-PSDB; ADF18446. GENBANK; J05147. WO2003089636-A1

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Gaps

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Indels

Length 1500;

58

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A gene encoding the milk protein bovien alpha-lactalbumin was isolated from a bovine genomic library. The bovine sequence consists of 2.0 kb of as flanking (control/chhancer) region, a 1.7 kb coding region and 8.8 kb of a 3' flanking region and 8.8 linto the vectors Pic 20R and Bluescript KS+. The alpha-lactalbumin 5' flanking control region cloned in the Ecosk site of pic 20R is given in AAQ37836 and AAQ37837. To understain the control of the control/enhancer region the 2.0 kbs of the 5' flanking region were sequenced (see AAQ37838). It has a signal peptide coding region in bps 1943-2043; a control region for alpha-lactalbumin at base 1966; a putative steroid response element at bps 1433-41446; and an RNA polymerase binding region at 1961-1978. (Updated on 25-MAR-2003 to correct PN field.)
polypeptide joined via a dipeptide linker to a C-terminal human beta-1,4-gladactostyltransferase 1 polypeptide (amino acids 49-389), with a C-terminal histidine tag. The fusion protein additionally has N-acetylgalactosaminyltransferase, lactosyltransferase and glucosyltransferase activities. Cells transfered with this gene are denoted Lec8/LG60 (KCTC 102239P), and can be used in the production of recombinant proteins having a LacdiNAc-R (GalNAc-beta 1,4-GlcNAc-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the control/enhancer region of the bovine alpha-lactalbumin plasmid pIC 20R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammary specific expression; alpha-lactalbumin; 5' flanking region; ss
                                                                                                                                                                                                                                                                                                                   CTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG
                                                                                                                                                                                                                                                                                                                                       Bovine alpha-lactalbumin genomic clone - promotes mammary specific expression of protein, e.g. insulin in mammalian milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2044;
                                                                                                                                                                                        Sequence 1500 BP; 370 A; 402 C; 366 G; 362 T; 0 U; 0 Other;
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nes 58; Conservative
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                                                                                                                                                                                                                                                                                                                   1 ATGATGTCCTTTGTC
                                                                                                                                                 glycoprotein structure.
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58; C
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04-JUL-1993
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AAQ37838
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                                       The present sequence is that of cDNA encoding bovine alpha-lactalbumin. The invention relates to a fusion protein, denoted alpha-LAGT ADF18450, comprising cattle alpha-lactalbumin and human beta 1,4-galactosyltransferase 1, that additionally has N-acetylgalactosaminyltransferase, lactosyltransferase and glucosyltransferase activities. Cells transfected with a gene ADF18449 encoding alpha-LAGT are denoted Lec8/LG60 (KCTC 10223BP), and can be used in the production of recombinant proteins having a LacdiNAc-R (GalNAc-hotal 1,4-GlcNAc-R) glycoprotein structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the coding sequence for a novel fusion protein, denoted alpha-LAGT, comprising an N-terminal bovine alpha-lactalbumin
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                                                                                                                                                                                                                                                                                                                                                                                                                       85
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glucosyltransferase, useful for producing recombinant glycoproteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-acetylgalactosaminyltransferase fusion protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha-lactalbumin;
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                                                                                                                                                                                                                                                                                                Score 58; DB 10; Length 724;
                                                                                                                                                                                                                                                     Sequence 724 BP; 182 A; 168 C; 163 G; 209 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; galactosyltransferase; enzyme; cattle; alpha-1
acetylgalactosaminyltransferase; lactosyltransferase;
glucosyltransferase; glycoprotein; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion protein comprising the activities of N-
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1. .57
/*tag= a
  Example 1; SEQ ID NO 1; 41pp; English.
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1. .1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADF18449 standard; cDNA; 1500 BP
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                                                                                                                                                                                                                                                                                                92.1%;
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Matches 58; Conservative
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P-PSDB; ADF18450.
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ADF18449;

RESULT 2 ADF1844

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retrovirus-based genomic screening; gene; ds.
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                  1979 ATGATGTCCTTTGTCTCTCTGCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG 2036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG 755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
         1 ATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG
                                                                                                                                                               beta-lactoglobulin; alpha S1-casein;
kappa-casein; lactoferritin; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cow; alpha-lactalbumin; vector; retroviral vector; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.1%; Score 58; DB 6; Length 2998;
100.0%; Pred. No. 2e-10;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2998 BP; 740 A; 679 C; 614 G; 965 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine alpha-lactalbumin gene retroviral vector.
                                                                                                                                           Yak milk protein gene related DNA sequence #8.
                                                                                                                                                                                                                                                                                                                                                                         Seven kinds of yak milk protein gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 8; 41pp; Chinese.
                                                                              ADE64697 standard; DNA; 2998 BP.
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                                                                                                                                                             yak milk; alpha-lactoalbumin;
alpha S2-casein; beta-casein;
                                                                                                                                                                                                                                                          08-DEC-2000; 2000CN-00134189
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Best Local Similarity 100.
Matches 58; Conservative
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P-PSDB; ADE64629.
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                                                                                                                                                                                             Bos grunniens
                                                                                                                                                                                                                                                                                                  (LINN/) LI N.
                                                                                                                       29-JAN-2004
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                                                                                                   ADE64697;
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'note= "Moloney murine leukaemia virus extended packaging
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'note= "human cytomegalovirus immediate early promoter"
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note= "bovine alpha-lactalbumin 3' flanking region"
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/note= "moloney murine leukaemia virus 3' LTR"
6649. .9009
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/note= "Moloney murine sarcoma virus 5' LTR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "bovine alpha-lactalbumin intron 1"
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                                                                                                                                                                                                              'product= "neomycin phosphotransferase'
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/note= "bovine alpha-lactalbumin exon
3658. .3714
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                          /*tag= q
/note= "LNC plasmid backbone"
Location/Qualifiers
1. .148
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26-MAR-2003; 2003US-00397569.
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/number= 3
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/label= attB2
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                                                                                                                                                                                                                                                              The present invention relates to a method of analysing genomic DNA clones which comprises providing a vector and a packaging cell, introducing the vector into packaging cell to transcribe the RNA molecule corresponding to the retroviral 5' and 3' long terminal repeats to produce a retroviral particle, transducing a cell line so that the RNA molecule is reverse transcribed and inserted into the genome of the cell line as a provirus, and analysing the provirus. The methods and compositions of the present invention are useful in functional genomics, particularly to the wexpression and screening of genomic DNA sequences encoding uncharacterised genes and protents. The present sequence is a vector used to demonstrate the method of the invention
                                                                                                                    Analyzing genomic DNA clones, useful in functional genomics, particularly to the expression and screening of genomic DNA sequences encoding uncharacterized genes and proteins, comprises retrovirus-based genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3658 ATGATGTCCTTTGTCTCTCTGCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG 3715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9009 BP; 2116 A; 2379 C; 2151 G; 2363 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.1%; Score 58; DB 10; Length 9009; 100.0%; Pred. No. 2.6e-10; tive 0; Mismatches 0; Indels 0
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/label=_s/_LTR
/label=_s/_LTR
/*tag=_b
/label=_Extended_packaging_region
                                           Imboden M, Eakle K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= hCMV promoter
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4442. .4466
/*tag= 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE64208 standard; DNA; 7472 BP
                                                                                                                                                                                                                             3xample 1; Fig 2; Opp; English.
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'label= aatB1
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/*tag≃ c
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2803. .3621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
  (GALA-) GALA DESIGN INC.
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                                        Bleck GT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 58; Conservat
                                                                                 WPI; 2003-788346/74.
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                                           Bremel RD,
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IID ADE6

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XXX BD 29---

XXX ADE7

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3727 AIGAIGICCTITGITTITTITTITTITTITTITTCCATGCCACCCAGGCCGAC 3786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a new antibody library which comprises at least vector expressing an antibody light or heavy chain. Antibodies are of increasing importance in human therapy, assay procedures and diagnostic methods and a need exists for efficient methods of generating and sorrening antibody libraries containing large numbers of antibodies. The antibody library of the invention over multiplicity of infection (MOI), and is useful in preparing a composition for diagnosing or treating a wide variety of disorders. The present sequence is the nucleic acid sequence of plaC-MALC, a GAREWAY retroviral vector containing DNA encoding the MNI4 antibody light chain, which was used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTGTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibody library comprising cells comprising at least one integrated retroviral vector expressing an antibody light or heavy chain, useful in preparing a composition for diagnosing or treating disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                    complement (6407. .7267)
                                                                                                                                                                                 /product= "b-Lactamase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 4; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-804051/75.
P-PSDB; ADE64202, ADE64204, ADE64200.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Impoden M;
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                                                                         /label= 3' LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-2002; 2002US-0368808P.
10-APR-2002; 2002US-0371299P.
28-MAR-2003; 2003US-00371299.
                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2003; 2003WO-US009662
4518. .5111
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Best Local Similarity 93.7
Matches 59; Conservative
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This invention relates to a new antibody library which comprises at least 100 cells, each of which comprises at least one integrated retroviral vector expressing an antibody light or heavy chain. Antibodies are of increasing importance in human therapy, assay procedures and diagnostic methods and a need exists for efficient methods of generating and screening antibody libraries containing large numbers of antibodies. The antibody library of the invention addresses this need, with the additional advantage of strict control over multiplicity of infection (MOI), and is useful in preparing a composition for diagnosing or treating a wide variety of disorders. The present sequence is the nucleic acid sequence of plac-Lilc, a GATEWAY retroviral vector containing DNA exception of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibody library comprising cells comprising at least one integrated retroviral vector expressing an antibody light or heavy chain, useful in preparing a composition for diagnosing or treating disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7490 BP; 1764 A; 2041 C; 1894 G; 1791 T; 0 U; 0 Other;
                                                                                                *tag= b
label= Extended_packaging_region
                                                                                                                                                                                                                                                                                                                                                                                       /label= 3' LTR
complement (6425. .7285)
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                                                                                                                                                                                                                   *tag= e
label= hCMV promoter
                                                                                                                                                                             *tag= d
|label= EM7_promoter
| 1804. .3621
                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                  *tag= g
product= "LL2 LC"
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                                                                                                                                         *tag= c
product= "Neo"
                                                           /*tag= a
/label= 5'_LTR
807. 1616
                                                                                                                                                                                                                                                           '*tag= f
'label= aatB1
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|abel= attB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-2002; 2002US-0368808P.
10-APR-2002; 2002US-0371299P.
28-MAR-2003; 2003US-00371299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAR-2003; 2003WO-US009662
                                                                                                                             660. .2454
                                                                                                                                                                  679. .1735
                                                                                                                                                                                                                                               625. .3649
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/label= AMP
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P-PSDB; ADE64202, ADE64203.
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            Unidentified
                                                                                                                                                                                                                                             misc_feature
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                                                                                      misc_feature
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                                                                                                                                                                                                                   Transgenic animal; weight gain; lactase activity; pathogen resistance; rotovirus; coronavirus; Escherichia coli; Salmonella; piglet development; bovine; porcine; human; insulin-like growth factor I; alpha lactalbumin; IGF-I; chimeric; LA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                /*tag= c
/note= "Bovine alpha-lactalbumin signal peptide coding
                                                                                                                                                                                                                                                                                                                                                            b
"Bovine alpha-lactalbumin transcription start
                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "Bovine alpha-lactalbumin 5' flanking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Bovine alpha-lactalbumin 3' end of exon 1"
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Length 7490;
                                                                                                                                                                                                                                                                                                                                                                                                                                            'product= "Human/Bovine/Porcine IGP-I protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                number= 1
'note= "Bovine alpha-lactalbumin intron 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Bovine alpha-lactalbumin intron 2"
3295. .3369
                   Indele
                                                                                                                                                                                                     Bovine alpha lactalbumin/IGF-I chimeric gene construct.
 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Bovine alpha-lactalbumin
1821. .3294
 Score 56.6; DB 10
Pred. No. 7.7e-10;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= e
note= "IGF-I stop codon"
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                       BP.
                                                                                                                                       AAD32015 standard; DNA; 4532
89.8%;
ilarity 93.7%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341. .2661
                                                                                                                                                                          (revised)
(first entry)
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 Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                         3787 ATC 3789
                                                                        61 AAC 63
                                                                                                                                                                                                                                                                   Bos sp.
Sus scrofa.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                          29-AUG-2003
18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                    misc_signal
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                                                                                                                                                         AAD32015;
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Bleck GT;
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                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to transgenic animals (e.g. pig) that express an increased milk volume and growth factors e.g. insulin-like growth factor increased milk volume and growth factors e.g. insulin-like growth factor milk. The invention also provides transgenic animals encoding a growth factor and/or alpha-lactalbumin (inA) operably linked to a mammary preferential promoter. The transgenic animals are useful for increasing the amount or volume of growth factor in milk, as well as for increasing the weight gain, intestinal lactase activity, intestinal cell division, intestinal villi length, and resistance to intestinal pathogens (e.g. rotovirus, coronavirus, Becherichia coli or Salmonella) in suckling animals. The transgenic animals are also useful for providing milk to facilitate piglet development, improve health and decrease piglet many/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howine/howin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transgenic animals (e.g. pig) that express an increased milk volume and growth factors in their milk, useful for increasing the weight gain or resistance to pathogens, or improving health in a suckling animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chimeric gene construct. (Updated on 29-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCCAGGCTG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                         /*tag= m
/note= "Bovine alpha-lactalbumin 3' flanking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4532 BP; 1168 A; 983 C; 1014 G; 1367 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4532;
                                                                            /note= "Bovine alpha-lactalbumin intron 3"
3874. .4203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
"Bovine alpha-lactalbumin exon 3"
                                                                                                                                                      /note= "Bovine alpha-lactalbumin exon
4204 4532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bleck GT, Monaco-Seigel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56.4; DB 6;
Pred. No. 8.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD28313 standard; DNA; 5691 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Fig 3; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.5%;
98.3%;
                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-2001; 2001WO-US025583
                     .3873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UNII ) UNIV ILLINOIS FOUND
                                                                                                                .4203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Donovan SM,
                                                                  number=
/note=
3370. ..
                                             *tag=
                                                                                                                                        *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 numan/bovine/porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-269186/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
tes 57; Conserv
                                                                                                                                                                                                                                                                                                 WO200214473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                    15-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wheeler MB,
                                                                                                                                                                                                                                                                                                                                            21-FEB-2002
                                                                                                                                                                                                        misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD28313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                       intron
                                                                                                                exon
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AAD2831
a
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Regulatory element; vector; erythropoietin; growth hormone; insulin;

Alpha-lactalbumin (LA) YP vector.

(first entry)

(revised)

07-AUG-2003 22-APR-2002

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*tag= c
product= "Bovine alpha-lactalbumin signal peptide coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product= "Bovine alpha-lactalbumin signal peptide coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel regulatory elements including nucleic acid encoding hybrid alpha-lactalbumin promoter or mutant RNA export element, for expressing one or more proteins e.g. antibodies, pharmaceutical proteins in host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel regulatory elements and vectors for the expression of one or more proteins in a host cell. The invention further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag= g
product= "Yersenia pestis light chain Fab gene coding
immunoglobulin, bone morphogenetic protein; interferon; interleukin; superoxide dismutase; T-cell receptor; surface membrane protein; WPRE; viral antigen; transport protein; addressin; regulatory protein; IRES; bovine; alpha-lactalbumin; promoter; ECMV; encephallomyocarditis virus; internal ribosome entry site; moloney murine leukemia virus; MoMuLV; woodchuck, mRNA processing enhancer; pre-mRNA processing enhancer; PPE;
                                                                                                                                                                                                                                                                                                                                                                                           'product= "Yersenia pestis heavy chain Fab gene coding
                                                                                                                                                                                                                                        /*tag= a
note= "Bovine/human alpha-lactalbumin 5' flanking
                                                                                                                                                                                                                                                                                                      /note= "Double mutated PPE sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "WPRE sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "MoMuLV 3' LTR"
                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 14; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "EMCV IRES
                                                                                                                                      Moloney murine leukemia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUN-2001; 2001WO-US020714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUL-2000; 2000US-0215851P.
                                                                                                                                                                                                                                                                             .2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .4441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .5052
                                                                                                                                                                                                                                                                                                                                                                                                                   .3742
                                                                                                                                                                                                                                                                                                                                                                   .3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .3799
                                                                                                                                                                                                                                                                                                                 .2459
                                                                                                   Encephalomyocarditis virus.
                                                                                                                                                                                                                                                                 region"
                                                                                                                                                                                                                                                                                                                                                      region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GALA-) GALA DESIGN INC
                                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                                                                                                         "egion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                  3167.
                                                                                                                                                                                                                                                                                                                    2403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-154749/20.
                                                                           human; chimeric; ds
                                                                                                                                                               Yersinia pestis.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200202783-A2
                                                                                                                                                      Marmota monax.
                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                              misc_feature
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provides methods of indirectly detecting the expression of a protein of interest. Comprising providing the host cell transfected with a vector encoding a polycistronic sequence comprising protein and a dealred protein operably linked by an internal ribosome entry site a dealred protein and culturing the host cell under suitable conditions so that the signal protein and the desired protein is produced, where the presence of signal protein and the desired protein is produced, where the presence of cignal protein indicates the presence of desired protein sequence. Cc signal protein indicates the presence of desired protein sequence of interest in a host cell. They are useful in the proteins of interest in a host cell. They are useful in the captors, hormone, insulin, immunoglobulins, protein C, cytokines and their receptors, hormones, von Willebrands factor, lung surfactant, serum albumins, DNSse, vascular endothelial growth factors receptors for a compare proteins, colony stimulating factors, interleukins, colony stimulating factors, interleukins, or proteins, colony stimulating factors, interleukins, viral superoxide dismutase, T-cell receptors, immunotoxins, bone morphogenetic proteins, colony stimulating factors, interleukins, viral antibodies, chimeric proteins, addressins, regulatory proteins, viral continularly useful for expressing G protein coupled receptors and other transport proteins, addressins, regulatory proteins, proteins in mammalian tissue culture host cells, including rat fibroblast colls, bovine kidney cells and human kidney cells. The present sequence provine alpha-lactalbumin land, heavy cells. The vector call bumin (Ma) Ye vector used in the invention. The vector sequence, bovine alpha-lactalbumin signal peptide, bovine alpha-lactalbumin signal peptide, bovine alpha-lactalbumin signal peptide, versenia pestis antibody heavy chain represent sequence, bovine alpha-lactalbumin signal peptide, versenia pestis antibody heavy chain represent sequence, bovine alpha-lactalbumin signal peptide, verse
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/product= "Bovine alpha-lactalbumin signal peptide coding

/*tag= g /product= "Yersenia pestis light chain Fab gene coding

.4441

CDS

*tag= region"

region"

/*tag= h /note= "WPRE sequence"

misc_feature

/note= "MoMuLV 3' LTR"

WO200202738-A2

murine leukemia virus

10-JAN-2002

'product= "Bovine alpha-lactalbumin signal peptide coding

/*tag= b /note= "Double mutated PPE sequence"

.2336

misc_feature

CDS

region"

a "Bovine/human alpha-lactalbumin 5' flanking

/product= "Yersenia pestis heavy chain Fab gene coding

.3137

CDS

*tag= region"

region"

/*tag= e
/note= "EMCV IRES"

.3799

CDS

*tag=

3167. .3742

misc_feature

*tag=

Sequence 5691 BP; 1384 A; 1443 C; 1435 G; 1429 T; 0 U; 0 Other;

ng enhancer (WPRE) sequence and 3' moloney murine l LTR. (Updated on 07-AUG-2003 to correct OS field.)

processing

(MOMulu)

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0
88.9%; Score 56; DB 6; Length 5691;
                            0; Indels
              No. 1.2e-09;
                            56; Conservative
             Local Similarity
 Query Match
                            Matches
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AAD28274 standard; DNA; 5691 BP.
                  (first entry)
                (revised)
                07-AUG-2003
22-APR-2002
          AAD28274;
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Alpha-lactalbumin (LA) YP vector.

Bovine; alpha-lactalbumin; promoter; pharmaceutical; industrial; ECMV; encephalomyocarditis virus; diagnostic; internal ribosome entry site; IRES; screening; moloney murine leukemia virus; MoMuLV; human; WPRE; woodchuck mRNA processing enhancer; pre-mRNA processing enhancer; PPE; chimeric; ds

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Moloney murine leukemia virus.
Marmota monax.
Encephalomyocarditis virus.
                                  Homo sapiens.
                       вов вр.
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Yersinia pestis. Unidentified. Chimeric

Location/Qualifiers Key misc_feature

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                                                             2403 ATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGC 2458
                    Gaps
                                               26
                                               1 ATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGC
100.0%; Pred. ....
                                                                         셤
                                               ઠે
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Bremel RD, Miller LU, Bleck GT,

(GALA-) GALA DESIGN INC

29-JUN-2001; 2001WO-US020710. 03-JUL-2000; 2000US-0215925P.

The invention relates to a host cell comprising a genome having at least two integrated integrating vectors. The integrating vectors comprise at least one excogenous gene operably linked to a promoter. The host cell is useful for producing a desired protein and for comparing protein functions. The host cells comprises a reporter gene which is from gene fluctions. The host cells comprises detecting a signal from the reporter gene. The desired protein includes proteins for pharmaceutical, indirectial, dagnostic and other purposes. The host cells is useful for indirectly detecting the expression of a desired protein, comprising providing the host cell transfected with a vector encoding a providing the host cell transfected with a vector encoding a polycistronic sequence comprising a signal protein and a desired protein is produced, where the presence of signal protein and the desired protein is produced, where the presence of signal protein and the desired protein is produced, where the presence of signal protein and indicates the presence of desired protein. The present sequence is alphate a lactabumin (LA) YP vector used in the invention. The vector comprises the following elements: 5' bovine/human alpha-lactabumin hybrid bovine alpha-lactabumin signal peptide, bovine alpha-LA signal peptide, bovine alpha-LA signal peptide, versenia pestis antibody heavy chain Fab coding region, Host cell for producing a desired protein and for screening compounds useful for pharmaceutical, industrial, diagnostic and other purposes, comprises multiple integrating vectors having an exogenous gene. Example 1; Fig 14; 191pp; English WPI; 2002-154737/20.

the scope of the invention.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a host cell comprising a genome comprising at least one integrated integrating vector, where the integrating vector comprises at least one exogenous gene operably linked to a promoter, and where the integrating vector lacks a gene encoding a selectable marker. The invention also relates to a method of transfecting host cells, involving providing a number of host cells comprising a genome and a number of integrating vectors, where the integrating vectors comprise at least one exogenous gene, and where the integrating vectors lack a gene encoding a selectable marker, contacting the host cell with a number of integrating vectors to generate transfected host cells comprising at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Integrating vectors to generate transferent most certs compitating at transfected host cells. The host cell is useful for producing a protein of integratest which involves providing a host cell, where the exogenous gene encodes a protein of interest and culturing the host cell under conditions such that the protein of interest is produced. The integrated exogenous gene is stable in the absence of selection. The integrating vector further comprises a secretion signal sequence operably linked to the exogenous gene. The host cell is useful for the production of proteins for pharmaceuticals and industrial, diagnostic and other purposes, and in the production of multiple variants of proteins, followed by analysis of the activity of the protein variants. This sequence represents alpha-lactalbumin (alpha-IA) YP vector DNA, used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pharmaceutical; industry; diagnosis; alpha-lactalbumin; alpha-LA; ds; YP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    purposes, comprising genome having at least one integrated vector having at least one exogenous gene and lacking selectable marker.
encephalomyocarditis virus (ECMV) IRES; bovine alpha-LA signal peptide Persenia antibody light chain Fab coding region, woodchuck mRNA processing enhancer (WRRE) sequence and 3' moloney murine leukemia virus (MoMuLV) LTR. (Updated on 07-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Host cell useful for producing proteins for pharmaceuticals, industrial
                                                                                                                                                                                                                                                                                2403 ATGATGTCCTTTGTCTCTGCTCGTGGTAGGCATCCTATTCCATGCCACCCAGGC 2458
                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                      ATGATGTCCTTTGTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGC
                                                                                                         Sequence 5691 BP; 1384 A; 1443 C; 1435 G; 1429 T; 0 U; 0 Other;
                                                                                                                                                 Score 56; DB 6; Length 5691;
Pred. No. 1.2e-09;
                                                                                                                                                                                           0; Indels
                                                                                                                                   88.9%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-lactalbumin (alpha-LA) YP vector DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eakle K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 11; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          York D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUN-2001; 2001US-00897511.
28-MAR-2002; 2002US-0368357P.
                                                                                                                                                                                                                                                                                                                                                                                          ADM68974 standard; DNA; 5691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2003; 2003US-00397079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                     Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GALA-) GALA DESIGN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-033957/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003224415-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM68974;
                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                     ADM68974
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The invention relates to a purified nucleic acid molecule associated with catation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, cappearing as ABX34636-ABX49947, or complements of them. Also included are appearing as ABX34636-ABX49947, or complements of them. Also included are included are acid linked to a promoter and a 3' non-translated sequence that the call to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and complements in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid acquences or its complement cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule, and (b) detecting the level or pattern of the complementary nucleic acid, where complementary nucleic acid september acid is predictive of the complementary nucleic acid is used for level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle
                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification;
                                                                                                                                                                                 2403 ATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGC 2458
                                                                                                                     Gaps
                                                                                                                                                          1 ATGATGTCCTTTTGTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine EST associated with lactation/muscle/fat deposition #290
                                  Sequence 5691 BP; 1384 A; 1443 C; 1435 G; 1429 T; 0 U; 0 Other;
                                                                                                                   .
0
                                                                          Length 5691;
                                                                                                                   Indels
                                                                          DB 12; L
1.2e-09;
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                                                                             Query Match

88.9%; Score 56; DB

Best Local Similarity 100.0%; Pred. No. 1.2

Matches 56; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; SEQ ID NO 290; 245pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tao N,
                                                                                                                                                                                                                                                                                                       ABX35125 standard; cDNA; 284 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JAN-1999; 99US-0115707P.
11-JAN-2000; 2000US-00480902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-2001; 2001US-00960352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Byatt JC, Mathialagan N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-110599/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2002137139-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAO N
                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos Taurus.
                                                                                                                                                                                                                                                                                                                                                  ABX35125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WARR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAON/)
                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                             SXG
                                                                                                                                                                                                  셤
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Novel regulatory elements including nucleic acid encoding hybrid alpha-lactalbumin promoter or mutant RNA export element, for expressing one or more proteins e.g. antibodies, pharmaceutical proteins in host cells.
                                 29-JUN-2001; 2001WO-US020714.
                                                     03-JUL-2000; 2000US-0215851P.
                                                                           (GALA-) GALA DESIGN INC
                                                                                                                     WPI; 2002-154749/20.
            10-JAN-2002
                                                                                                  Bleck GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD28267
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breeding, preparation of constructs for use in cattle gene expression, or
          for genetically improving cattle. The present sequence is one of the 15112 bovine LMPD EXT expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                        immunoglobulin; bone morphogenētic protein; interferon; interleukin; superoxide dismutase; T-cell receptor; surface membrane protein; CWV; viral antigen; transport protein; addressin; regulatory protein; ECWV; encephalomyocarditis virus; internal ribosome entry site; IRES; bovine; cytomegalovirus; moloney murine leukemia virus; MoMuLV; chimeric; alpha-lactalbumin; promoter; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
/note= "MN14 antibody heavy chain gene signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag= e
note= "Bovine alpha-lactalbumin signal peptide start
                                                                                                                                                       106 ATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Regulatory element; vector; erythropoietin; growth hormone; insulin;
                                                                                                                                          4 ATGICCTITIGICICTCTGCTCGTAGGCAICCTAITCCAIGCCACCCAGGCTG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= c
Notc= "MN14 antibody heavy chain gene start codon"
2271. .3846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= g
/note= "MN14 antibody heavy chain gene stop codon"
                                                                                                                        ö
                                                                                              Length 284;
                                                                                                                     0; Indels
                                                                           Sequence 284 BP; 71 A; 70 C; 74 G; 69 T; 0 U; 0 Other;
                                                     segdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                              87.3%; Score 55; DB 8; Le
100.0%; Pred. No. 1.3e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .. .812
*tag= a
'note= "CMV promoter/enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= h
/note= "MoMuLV 3' LTR'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag= d
note= "EMCV IRES"
                                                                                                                                                                                                                                                                                       Cytomegalovirus (CMV) MN14 vector.
                                                                                                                                                                                                                     AAD28306 standard; DNA; 4207 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                  Moloney murine leukemia virus.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .2846
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                                                                                                                                                                                                                                                                                                                                                                                                   Encephalomyocarditis virus.
                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .855
                                                                                                                    55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257.
                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200202783-A2
                                                                                                                                                                                                                                                                 22-APR-2002
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                                                                                                                                                                                                                                             AAD28306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter
                                                                                                                    Matches
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The invention relates to novel regulatory elements and vectors for the expression of one or more proteins in a host cell. The invention further provides methods of indirectly detecting the expression of a protein of interest, comprising providing the host cell transfected with a vector encoding a polycistronic sequence comprising a signal protein and a cesired protein operably linked by an internal ribosome entry site (IRES), and culturing the host cell under suitable conditions so that the signal protein and the desired protein is produced, where the presence of signal protein indicates the presence of desired protein. Regulatory elements and vectors of the invention are useful for the expression of proteins of interest in a host cell. They are useful for producing an immunoglobulin (Ig), preferably secretory Ig. They are useful in the expression of one or more proteins such as erythropotetin, growth commons, von Willebrands factor, lung surfactant, serum abumins, DNase, vascular endothelial growth factor, receptors for hormones or growth factors, immunotoxins, bone morphogenetic protein, interferons, colony stimulating factors, interleukins, surfactors, viral surfactures, viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2847 ATGGCCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGAC 2906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigens, transport proteins, addressins, regulatory proteins, antipodies, chimeric proteins and their fragments. The vectors are particularly useful for expressing G protein coupled receptors and other transmembrane proteins. The retroviral vectors are useful for expressing proteins in mammalian tissue culture host cells, including rat fibroblast cells, browine kidney cells and human kidney cells. The present sequence is cycomegalovirus (CMV) MNI4 vector used in the invention. The vector comprises the following elements: CMV promoter, MNI4 antibody heavy chain signal peptide, MNI4 antibody heavy chain, encephalomycoarditis virus (ECMV) IRES -bovine alpha-lactalbumin signal peptide, MNI4 antibody light chain and 3' moloney murine leukemia virus (MOMLUV) LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGATGICCTTTGICTCTGTCTGGTAGGCATCCTATTCCATGCCACCCAGGCTGTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.2%; Score 51.8; DB 6; Length 4207;
88.9%; Pred. No. 3.4e-08;
iive 0; Mismatches 7; Indels 0.
Example 1; Fig 7; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD28267 standard; DNA; 4207 BP.
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indirectly detecting the expression of a desired protein, comprising providing the host cell transfected with a vector encoding a polycistronic sequence comprising a signal protein and a desired protein operably linked by an internal tribosome entry site (IRES), and culturing the host cell under suitable conditions so that the signal protein and the desired protein is produced, where the presence of signal protein and indicates the presence of desired protein. The presence of signal protein cytomegalovirus (CWV) MN14 vector used in the invention. The vector comprises the following elements: CWV promoter, MN14 antibody heavy chain signal peptide, MN14 antibody heavy chain, encephalomyocarditis virus (ECWV) IRES -bovine alpha-lactalbumin signal peptide, MN14 antibody light chain and 3' moloney murine leukemia virus (MoMuLV) LTR

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Sequence 4207 BP; 1030 A; 1202 C; 1058 G; 917 T; 0 U; 0 Other;

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Gaps ; 0

82.2%; Score 51.8; DB 6; Length 4207; 88.9%; Pred. No. 3.4e-08; ive 0; Mismatches 7; Indels 0;

Conservative

Local Similarity

Query Match

26;

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Bovine, alpha-lactalbumin, promoter, pharmaceutical, industrial, ECWV, encephalomyocarditis virus, diagnostic, internal ribosome entry site, IRES, screening, CMV, cytomegalovirus, moloney murine leukemia virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Host cell for producing a desired protein and for screening compounds useful for pharmaceutical, industrial, diagnostic and other purposes, comprises multiple integrating vectors having an exogenous gene.
                                                                                                                                                                                               /*tag= b
/note= "MN14 antibody heavy chain gene signal peptide
                                                                                                                                                                                                                                                                                              *tag= e
'note= "Bovine alpha-lactalbumin signal peptide start
                                                                                                                                                                                                                                                                                                                                    /*tag= f
/note= "First codon mature MN14 antibody light chain
                                                                                                                                                                                                                                      '*tag= c
'note= "MN14 antibody heavy chain gene start codon"
                                                                                                                                                                                                                                                                                                                                                                           /*tag= g
/note= "MNI4 antibody light chain gene stop codon"
                                                                                                                                                       1. .812
/*tag= a
/note= "CMV promoter/enhancer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   York
                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= h
/note= "MoMuLV 3' LTR"
                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                 *tag= d
note= "EMCV IRES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bleck GT,
         Cytomegalovirus (CMV) MN14 vector.
                                                                                           Cytomegalovirus.
Moloney murine leukemia virus.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-2001; 2001WO-US020710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUL-2000; 2000US-0215925P.
                                                                                                                                                                                                                          .2259
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                                                                                                                                                                                                                                                         .2846
                                                                                                                                                                                                                  start codon'
                                                                                                                                                                                                                                                                                                                           .2906
                                                                                                                                                                                                                                                                                     .2849
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                                                                           Encephalomyocarditis virus.
                                                                                                                                                                                     .855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miller LU,
                                                                                                                                                                                                                                                                                                                                                                3543.
                                                          MoMuLV; chimeric; ds.
                                                                                                                                                                                      853.
                                                                                                                                                                                                                                                                                      847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-154737/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200202738-A2
                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                     misc_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bremel RD,
                                                                                                                            Chimeric.
                                                                                                                                                          promoter
                                                                                        Sp.
                                                                                                                                                                                                                                                                                                                                                                                             LTR
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2847 ATGGCCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGAC 2906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Host cell useful for producing proteins for pharmaceuticals, industrial purposes, comprising genome having at least one integrated vector having at least one exogenous gene and lacking selectable marker.
1 ATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTGTT
                                                                                                                                                                                                                                                                                                                                     Pharmaceutical; industry; diagnosis; CMV MN14 vector; CMV; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eakle K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 4; 78pp; English.
                                                                                                                                                                                            ADM68967 standard; DNA; 4207 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          York D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2003; 2003US-00397079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUN-2001; 2001US-00897511.
28-MAR-2002; 2002US-0368357P.
                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GALA-) GALA DESIGN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bremel RD, Bleck GT,
                                                                                                                                                                                                                                                                                                      CMV MN14 vector DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-033957/03.
                                                                                                       2907 ATC 2909
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                                                                    61 AAC 63
                                                                                                                                                                                                                                                                  03-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                               ADM68967;
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The invention relates to a host cell comprising a genome having at least two integrated integrating vectors. The integrating vectors comprise at least one exogenous gene operably linked to a promoter. The host cell is useful for producing a desired protein and for comparing protein functions. The host cells comprises a reporter gene which is from gene fluorescent protein, luciferase, beta-galactosidase and beta-lactamase, and the assaying step further comprises detecting a signal from the reporter gene. The desired protein includes proteins for pharmaceutical, industrial, diagnostic and other purposes. The host cells is useful for

Example 1; Fig 7; 191pp; English.

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least one integrated copy of the integrating vector and selecting the transfected host cells. The host cell is useful for producing a protein of interest which involves providing a host cell, where the exogenous gene encodes a protein of interest and culturing the host cell under conditions such that the protein of interest is produced. The integrated vector further comprises a stable in the absence of selection. The integrating vector further comprises as excretion signal sequence operably linked to the exogenous gene. The host cell is useful for the production of proteins for pharmaceuticals and industrial, diagnostic and other purposes, and in the production of multiple variants of proteins, followed by analysis of the activity of the protein variants. This sequence represents CMV MN14 vector DNA, used in the scope of the
                                                                                                                                                                                                                                                                                                                                                                                       invention.
         8888888888888888888
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Sequence 4207 BP; 1030 A; 1202 C; 1058 G; 917 T; 0 U; 0 Other;

1 ATGATGTCCTTTGTCTCTTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTGTT 60 0; Gaps Query Match
Best Local Similarity 88.9%; Pred. No. 3.4e-08;
Matches 56; Conservative 0; Mismatches 7; Indels 0; ò

2847 ATGCCTCCTTTGTCTCTCTCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGAC 2906

61 AAC 63

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2907 ATC 2909

Search completed: October 1, 2005, 13:37:30 Job time : 373.982 secs

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338773 BA 172963 BA 172963 BA 160077 BA 160706 BA 343349 BA 337857 BA 337857 BA 231984 BA 231987 BA 231988 BA

BE485759
BE478560
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BG691240
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BG681304
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BG69160

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OM nucleic

Run on:

Sequence:

Searched:

Database

Result Š

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Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="pooled"
/lab.host="DH10B"
/clone_lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease states."
                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 140)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
Analysis of bovine mammary gland EST and functional annotation of
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                      ывчезгээ 140 bp mRNA linear
169315 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
BE483233
                                                                                                                                                                                                                                                                                                                                                                                                                         the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
22135956
                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .140
/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACKWARD: GTTTTCCCAGTCACGACG
Plate: 13 row: I column: 19
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9913"
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BE477066
BG693240
BE588671
BG689677
BG691002
BE588483
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BG693331
BG692696
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BF230828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                         BE483233.1 GI:9602766
                                                                                                                                                                                                                                                                                                                           Bos taurus (cow)
Bos taurus
12140684
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                        RESULT 1
BE483233
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
PUBMED
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE485405 172423 BG687739 334959 BB58484668 171408 BE588964 194651 BE589398 195533 BE482872 168810 BG690289 338769 E
                                                               October 1, 2005, 13:13:06; Search time 2924.2 Seconds (without alignments) 820.069 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                           1 atgatgtcctttgtctctct......atgccacccaggctgttaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE487063
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                           34239544 segs, 19032134700 residues
                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF230700
BG687704
BB482526
BF230601
BG693834
BE485596
BF230784
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BE589398
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                                                      US-10-820-777-1
63
                                                                                                                                                                                                                                                                                               gb_est1::
gb_htc::*
gb_est4::*
gb_est4::*
gb_est6:::
gb_gss1::*
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3219
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Match
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                                                                                                                                               Scoring table:
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EST 27-MAR-2003

BM878960 BF230828

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Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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/lab_host="DH10B"
/clome llb="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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1 (bases 1 to 161)

2 Sostegard,T., Capuco,A.V., White,J., Van Tassell,C.P., Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D. and Quackenbush,J.
                                                                                                                                                                                                                                                           Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index.

Mamm. Genome 13 (7), 373-379 (2002)
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the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
                                                                                                         Chordata, Craniata, Vertebrata, Euteleostomi,
Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                         1 (bases 1 to 149)
Sonstegard, T. Capuco, A.V., White, J., Van Tassell, C.P.,
Comnor, B. B., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
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                                                                                                                                                                                                                                                                                                                                                                                              USDA, ARS, Beltsville Agricultural Research Center Bd1g. 200 Rm 2A, Beltsville, MD 20705, USA TTE1: 301 504 8416 Fax: 301 504 8414
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100.0%; Pred. No. 4.5e-09;
iive 0; Mismatches 0;
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 125 row: L column: 2
Seg primer: ATTTAGGTGACACTATAG
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/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                              Contact: Sonstegard TS
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BE589418.1 GI:9842457
                    GI:9606596
                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                  Bos taurus (cow)
                                                                                                                                                         Bovinae; Bos.
                  BE487063.1
                                                                                       Bos taurus
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BE589418
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USDA, ARS, Beltsville Agricultural Research Center
Belg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRimmerch 12 options.
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/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
/incre="Vector pcMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bovinae; Bovinae; Bovinae; Consess 1 to 145)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P., and Quackenbush, J. Sultana, R., Shade, L., Wray, J.E., Wells, K.D. and Quackenbush, J.
                                                                                                                                  28
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                                    92.1%; Score 58; DB 2; Length 140; 100.0%; Pred. No. 4.4e-09; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                     BE479481 145 bp mRNA linear 164191 BARC 5BOV BOS taurus CDNA 5', mRNA sequence.
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Mamm. Genome 13 (7), 373-379 (2002)
22135956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACKWARD: GTTTTCCCAGTCACGACG
Plate: 139 row: D column: 7
Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH108"
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                                                                                    Conservative
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Bos taurus
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58; Conserv
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BE487063
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BE479481
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Indels

28 Gaps

EST 27-MAR-2003

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EST 27-MAR-2003

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Email: tadesolpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                      /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
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/lab host="DH10B"
/clone_lib="BARC SBOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Analysis of bovine mammary gland EST and functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 321)
Sonsteady T., Capuco, A.V., White, J., Van Tassell, C.P.,
Comnor, E. E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
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                                                                                                                                                                                                                                                                                                                                                   Length 209;
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334904 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
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USDA, ARS, Beltsville Agricultural Research Center
Bdg. 200 Rm. 2A, Beltsville, MD 20705, USA
Tel: 301 504 8414
                                                                                                                                                                                                                                                                                                                                              92.1%; Score 58; DB 2; Lv 100.0%; Pred. No. 4.7e-09; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
22135956
                                                                                        /mol_type="mRNA"
/db_xref="taxon:9913"
/tisuue_type="pooled"
/lab_host="DH10B"
/clone_lib="BARC_5BOV"
                                                    1. .209
/organism="Bos taurus"
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Plate: 33 row: D column: 3
Seg primer: ATTTAGGTGACACTATAG.
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Seg primer: ATTTAGGTGACACTATAG
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/db xref="taxon:9913"
                          Location/Qualifiers
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KEYWORDS
SOURCE
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                                                                                                                                                      Email: tade@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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Bd1g. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 S04 8416
Fax: 301 504 8416
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="BARC 5BOV"
hote="Vector: pCNV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 161;
                                           Contact: Sonstegard TS
USDA, ARS, Beltaville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltaville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.1%; Score 58; DB 2; Le llarity 100.0%; Pred. No. 4.5e-09; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                      Plate: 120 row: L column: 23
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
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BACKWARD: GTTTTCCCAGTCACGACG
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58; Conserv
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                          2140684
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Best Local
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8

ACCESSION

BG693760 LOCUS

RESULT 7

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AUTHORS

JOURNAL

TITLE

FEATURES

REFERENCE

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12140684
Contact: Sonstegard TS
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Balga. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
/incte="Vector pcoled mRNA isolated from mammary
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
                                                                                                                                          Johnson, 200.

Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
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22135956
12140684
                                                                                Chordata, Craniata, Vertebrata, Euteleostomi,
Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 330)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
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5.1e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACKWARD: GTTTTCCCAGTCACGACG
Plate: 11 row: A column: 14
Seg primer: ATTTAGGTGACATATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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PCR PRimers
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                                                                                                     Mammalia; Eutheria;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                     Eukaryota; Metazoa;
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                                           taurus (cow)
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22135956
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BF230601
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Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="pooled"
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/clone_lib="BARC_SBOV"
/note="Vector: pCMV_SPORT6; Site_1: NotI; Site_2: SalI;
/note="Vector: pCMV_SPORT6; Site_1: NotI; Site_2: SalI;
/ibtrary made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
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Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P., Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D. and Quackenbush, J.
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                                                                                                     1 ATGATGTCCTTTGTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG 58
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                                                                                                                                                                                                                                                  326 bp mRNA linear
344282 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
BG693760
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                  Score 58; DB 4; Length 321;
Pred. No. 5.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USDA, ARS, Beltsville Agricultural Research Center Bdlg. 200 Rm. 2A, Beltsville, MD 20705, USA TEL: 301 504 8416 Fax: 301 504 8414
                                                         0; Indels
92.1%; Scor.
100.0%; Pred. No. 5.-
'-- 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
22135956
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Location/Qualifiers
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/db_xref="taxon:9913"
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 47 row: N column: 7
                                                                                                                                                                                                                                                                                                                            BG693760.1 GI:13935580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Sonstegard TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 326)
                                    . Similarity 100.
58; Conservative
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Best Local Similarity
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EST 27-MAR-2003

RESULT 8 BE482526 LOCUS

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us-10-820-777-1.rst

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/clone_lib="BARC 5BOV"
hote="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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/lab host="DH10B"
/clore lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 343)
Sonsteadard, T. Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                         13 AIGAIGICCTITGICTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG 70
                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE477471 343 bp mRNA linear
161184 BARC 5BOV Bos taurus CDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                    Length 340;
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Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
121: 301 504 8416
Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                       DB 4; Le
5.1e-09;
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                                                                                                                                                                                                                                                                                                    92.1%; Score 58; DB
100.0%; Pred. No. 5.1
ive 0; Mismatches
                        organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACKWARD: GTTTTCCCAGTCACGACG
Plate: 3 row: G column: 21
Seg primer: ATTTAGGTGACACTATAG.
                                                /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                            /tissue_type="pooled"
/lab_host="DH108"
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                                                                                                                                                                                                                                     states."
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Best Local Similarity
Matches 58; Conserv
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Best Local Similarity
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22135956
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ACCESSION
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ORGANISM
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BE477471
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MEDLINE
PUBMED
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KEYWORDS
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                 USDA, ARS, Belteville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8416
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904e. Vector identified by cross_match with the -minscore 18
PCR PRimers
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Bd19. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8416
Fax: 301 504 8414
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
/ibrary made from pooled mRNA isolated from mammary
Lissues at eight physiological, developmental, and disease
states."
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 340)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D. and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.1%; Score 58; DB 2; Length 330; 100.0%; Pred. No. 5.1e-09; ive 0; Mismatches 0; Indels
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344386 BARC 5BOV Bos taurus CDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 47 row: 0 column: 15
Seg primer: ATTTAGGTGAACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                           FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGCACG
Plate: 109 row: D column: 5
Seg primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="pooled"
/lab_host="DH108"
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Contact: Sonstegard TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Sonstegard TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58; Conservative
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SOURCE
ORGANISM
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BG693834
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PUBMED
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Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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/lab_host="DH10B"
/clone_lib="BARC SBOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                   Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
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Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Sonort, E.B., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
Analysis of bovine mammary gland EST and functional annotation of
                      Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                  1 (bases 1 to 386)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Comnor, E. E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
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USDA, ARS, Beltsville Agricultural Research Center
Bd19. 200 Rm 2A, Beltsville, MD 20705, USA
T=1: 301 504 8414
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Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
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100.0%; Pred. No. 5.2e-09
:ive 0; Mismatches C
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Mamm. Genome 13 (7), 373-379 (2002)
22135956
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/organism="Bos taurus"
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BACKWARD: GTTTCCCAGTACAGGACG
Plate: 109 row: P column: 5
Seg primer: ATTAGGTGACACTATAG.
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/db_xref="taxon:9913"
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                    Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovinae; Bos.
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USDA, ARS, Beltsville Agricultural Research Center
Balgo. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@lpai.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRimmers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pooled"
/lab host="DH10B"
/clone lib="BARC SBOV"
/note="Vector: pCMV SDOYR6; Site_1: Not1; Site_2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 375)
Sonstegard,T., Capuco,A.V., White,J., Van Tassell,C.P.,
Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
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                                              28
                                                              13 ATGATGTCCTTTGTCTCTCTGCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG 70
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                                          1 ATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTG
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                                                                                                                                                                                         BE485596 375 bp mRNA linear 172678 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
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252656 BARC 5BOV Bos taurus CDNA 5', mRNA sequence.
BF230784
0; Indels
  0; Mismatches
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/db_xref="taxon:9913"
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BACKWARD: GTTTTCCCAGTCACGAC
Plate: 132 row: A column: 13
Seg primer: ATTTAGGTGACACTATAG.
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Bos taurus (cow)
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                 Tel: 301 504 8416

Pax: 301 504 8414

Email: tadsolpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
pcr PRimers
                                                                                                                                                                                                                                                                                                                                                                                          /clome lib="BARC SBOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled mRNA isolated from mammary
Lissues at eight physiological, developmental, and disease
states."
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E. B., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGAIGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCAGGCTG 58
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338933 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
BG690404
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USDA, ARS, Beltsville Agricultural Research Center
Bd1g. 200 Rm. 2A, Beltsville, MD 20705, USA
TF1: 301 504 8414
Fax: 301 504 8414
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
22135956
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Seq primer: ATTTAGGGTGACACTATAG.
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Plate: 37 row: E column: 15
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/db_xref="taxon:9913"

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/lab_host="DAIDB"

/clone_lib="BARC_5BOV"

/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;

Library made from pooled mRNA isolated from mammary

Lissues at eight physiological, developmental, and disease
states."
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Query Match 92.1%; Score 58; DB 4; Length 395; Best Local Similarity 100.0%; Pred. No. 5.3e-09; Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps

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Search completed: October 1, 2005, 15:37:39 Job time : 2926.2 secs

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                                                                       October 1, 2005, 13:15:56; Search time 111.504 Seconds
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-930-3778-1

US-09-949-016-3019

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US-09-949-016-1318

US-09-949-016-17033

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Maximum Match 100%
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                                              OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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194937
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Match Length
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No.
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Sequence 186, App
Sequence 150, App
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14853, A
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17162, A
14837, A
32, Appl
205793,
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GENERAL INFORMATION:
APPLICANT: BLECK, GREGORY T.
APPLICANT: BLECK, GREGORY T.
APPLICANT: BLECK, GREGORY T.
APPLICANT: BLECK, ROBERT D.
TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE
TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE
TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE
TITLE OF INVENTION: DAPPA-LACTALBUMIN AND METHODS OF USE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ANDRESS:
CORRESPONDENCE NESCONSIN AVE., SUITE 1100
STATE: WILMAUKEE
STATE: WILMAUKEE
STATE: WILMAUKEE
STATE: WILMAUKEE
STATE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALCANTIN ROBERS: US/OS/M1, 601
FILTH OF THE OFFICE 
             US-09-252-991A-10342
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US-09-261-970-1
US-09-949-016-17162.
US-09-949-016-17162.
US-09-949-016-205793
US-09-922-540-948
US-09-949-016-17550
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/744,765
FILING DATE:
ATTORNEY/GENT INFORMATION:
NAME: Sara, Charles S
REGISTRATION NUMBER: 30,492
REGISTRATION NUMBER: 30,492
REGISTRATION NUMBER: 30,492
REGISTRATION NUMBER: 30,492
RELEPHONE: (608) 255-202
TELEPHONE: (608) 255-2182
TELEFAX: (608) 255-2182
TELEXX: 26932 ANDSTARK
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2044 base pairs
TYPE: MUCIEIC acid
STRANDEDNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 3, Application US/08071601; Patent No. 5530177
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1482
14101
87690
271134
305491
1254
                       552
6717
175
13533
86380
118999
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; NAME/KEY:
; LOCATION:
US-08-621-100-3
                                                                             Query Match
                                                                                                Best Loca
Matches
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                                                                                                                                               Query Match 92.1%; Score 58; DB 1; Length 2044; Best Local Similarity 100.0%; Pred. No. 2.6e-11; Matches 58; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08621100
Patent No. 585000
GENERAL INFORMATION:
APPLICANT: BLECK, GREGORY T.
APPLICANT: BREMEL, ROBERT D.
TITLE OF INVENTION: ALPHA-LACTALBUMIN AND METHODS OF USE NUMBER OF SUGUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inherited control region for a-lactalbumin 1966
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/621,100
FILING DATE: 22-MAR-1996
CLASSIFICATION: 800
                      putative steroid response element 1433..1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL.
STREET: 100 E. WISCONSIN AVE., SUITE 1100
CITY: MILWAUKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      putative steroid response element 1433..1446
                                                                         RNA polymerase binding region 1961..1978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY JOATE:
NAME: SAZA, CHARIES S.
NAME: SAZA, CHARIES S.
REGISTRATION NUMBER: 30,492
RECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-202
TELEPHONE: (608) 255-2182
TELERS: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRACATER.STICS:
LENGTH: 2044 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/744,765
FILING DATE:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 53202-4178
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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LOCATION:
FEATURE:
FEATURE:
NAME/KEY:
LOCATION:
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LOCATION:
                                                                       NAME/KEY:
COCATION:
US-08-071-601-3
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FEATURE:
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US-08-621-100-3
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                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence:alpha-LA/IGF-I; OTHER INFORMATION: gene construct
US-09-930-377B-1
                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09930377B

Patent No. 6677500

GENERAL INFORMATION:
APPLICANT: Wheeler, Matthew B.
APPLICANT: Black, Gregory T.
APPLICANT: Black, Gregory T.
APPLICANT: Monaco-Seigel, Marcia
TITLE OF INVERTION: Animals Expressing Exogenous IGF-I in their Milk FILE REFERENCE: 66-00

CURRENT APPLICATION: NUMBER: US/09/930,3778

CURRENT FILING DATE: 2001-08-15

PRIOR FILING DATE: 2000-08-15
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                                                                                                   Length 2044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Alpha-lac Albumin Gene Constructs
NUMBER OF SEQUENCES: 17
NUMBER OF SEQUENCES: 17
NUMBER OF SEQUENCES: 17
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2119 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                Match 92.1%; Score 58; DB 2; Le Local Similarity 100.0%; Pred. No. 2.6e-11; es 58; Conservative 0; Mismatches 0;
RNA polymerase binding region 1961..1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-381-691-17; Application US/08381691; Sequence 17, Application US/08381691; Patent No. 5852224; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4532
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MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO
US-08-381-691-17
                                                                                                                                                                                                                                                                                                                                                                US-09-930-377B-1
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Sequence 107, Application US/09536784

Patent No. 6573082

GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Choi et. al.
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                            2390 ricriccirrescricitedeasescriescriricassaracceasscrir 2342
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GGTAGGCATCCTATTCCATGCCACCCAGGCTGT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                 CUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
41.3%; Score 26; DB.
Best Local Similarity 70.0%; Pred. No. 6.9;
Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 98340P2
TELECOMMUNICATION INFORMATION:
                                                                                                                             US-08-961-083-107/c
; Sequence 107, Application US/08961083
; Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 593 DARM TO TUBE SEQUENCE CHARACTERISTICS: LENGTH: 593 DARM TO TUBE SEQUENCE CHARACTERISTICS: LENGTH: 593 DARM TO TUBE SECUENCE SEQUENCE SEQUENCE SEQUENCE SE
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Maryland COUNTRY: USA
11 TIGICICICICCICC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-536-784-107/c
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-01-0-31
PRIOR FILING DATE: 2000-01-0-31
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                     US-09-949-016-3019/c
; Sequence 3019, Application US/09949016
; Fatent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.;
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 TIGICICICICCICCIGGIAGCAICCIATICCATGCCACCCAGGCIGT 59
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                        Length 2119;
                   Score 41.6; DB 2;
Pred. No. 2.2e-05;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/09949016; Patent No. 6812339; GENERAL INFORMATION:
                      Query Match
Best Local Similarity 83.9%;
Matches 47; Conservative
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Best Local Similarity 71.4%;
Matches 35; Conservative
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Best Local Similarity 71.4%;
Matches 35; Conservative
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CRGANISM: Human
US-09-949-016-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-09-949-016-12/c
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LENGTH: 2891
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Pred. No. 6.9;
0; Mismatches 15; Indels
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; Sequence 1, Application US/08928284
; Fatent No. 5882871
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION: ein
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
                                                                                   APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIPICATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FasteSO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,284
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 107:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 60/026,682
FILING DATE: 24-8EP-1996
ATTORNEY AGENT INFORMATION:
NAME: Dickinson, Q. Todd
REGISTRATION NUMBER: 28,354
REFERRNCE DOCKET NUMBER: P50543
TELECOMMUNICATION INFORMATION:
TELECHONE: 21/994-2252
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 593 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 107:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.0%;
Matches 35; Conservative
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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FOR DIAGNO
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APPLICANT: Lynn Doucette-Stamm et al.
APPLICANTON: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus TITLE OF INVENTION: PREMORE: US/09/583,110
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: US 60/085,131
PRIOR FILING DATE: US 60/051,553
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 1642
LENGTH: 1506
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Patent No. 6800744

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                                                                                                                Gaps
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                                                                                                                                             Score 26; DB 2; Length 876; Pred. No. 7.7; 0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM
COMPUTER: CD/ROM
COMPUTER: < Unknown>
OPERATING SYSTEM: <Unknown>
CURRENT APPLICATION DATA:
FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.3%; Score 26; DB ilarity 70.0%; Pred. No. 9; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1642, Application US/09583110 Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Streptococcus pneumoniae
US-09-583-110-1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                             41.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS
LENGTH: 876 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                    Best_Local Similarity 70.0
Matches 35; Conservative
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Best Local Similarity
Matches 35; Conserv
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US-09-583-110-1642/c
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                                                                                                US-08-928-284-1
                                                                                                                                                Query Match
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SEQUENCE CHARACTERISTICS:
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; ORGANISM: Human
US-09-949-016-69680
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ORGANISM: Human
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LENGTH: 601
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Parent No. 6420135

GENERAL INFORMATION:
APPLICANT: CLARIES KUNSCH
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
             APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ATIOIBLIO, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (701)893-507
INFORMATION FOR SEQ ID NO: 2390:
SEQUENCE CHARACTERISTICS:
LENGTH: 1515 base pairs
TYPE: NUCLeic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (B) LOCATION 1..1515
SEQUENCE DESCRIPTION: SEQ ID NO: 2390:
US-09-107-433-2390
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ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHON FOR SEQ ID NO: 167:
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
PRIOR APPLICATION DATA:
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ORIGINAL SOURCE:
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Matches 35
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GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR PELICATION NUMBER: 60/241,755
PRIOR PELICATION NUMBER: 60/231,768
PRIOR PELICATION NUMBER: 60/231,498
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESOF FOR WINDOWS VERSION 4.0
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Sequence 69681, Application US/09949016

Patent No. 6812339

CENERAL INFORMATION:

TITLE OF INVENTION: PUTPH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL0001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09

PRIOR PILING DATE: 2000-09

PRIOR PILING DATE: 2000-09

SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                               41.3%; Score 26; DB 3; Length 9711; 70.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24.8; DB 4; Length 6 Pred. No. 19; 0; Mismatches 17; Indels
                                                                                                                                                                                                                         0; Mismatches
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; Sequence 69680, Application US/09949016
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Best Local Similarity 70.03
Matches 35; Conservative
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Best Local Similarity 67.3
Matches 35; Conservative
LENGTH: 9711 base pai
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                 ; TOPOLOGY: linear
US-08-961-527-167
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US-09-949-016-69681

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RESULT 15

US-09-949-016-16317/c

Sequence 16317, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORE ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16317

LENGTH: 28136
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                                                                                                                   128 IGTCCAGTGTTTCACTGCCTCCTGAGTCCTTTATGCCTTGGCACCCAGGC 77
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39.4%; Score 24.8; DB 4; Length 601; 67.3%; Pred. No. 19; tive 0; Mismatches 17; Indels
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Pred. No. 55;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LOCATION: (1)...(28136)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16317
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Best Local Similarity 67.3%;
Matches 35; Conservative
Query Match
Best Local Similarity 67.3
Matches 35; Conservative
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ORGANISM: Human
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Search completed: October 1, 2005, 15:41:11 Job time : 113.504 secs

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JS-10-397-569-1
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Sequence 4, Appli
Sequence 3, Appli
                                                                                                                     October 1, 2005, 13:26:16 ; Search time 587.628 Seconds (without alignments) 740.253 Million cell updates/sec
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Fublished Applications_Nay.

(cgn2_6/ptodata/2/pubpna/US07_PUBCCMB.seq:*

(cgn2_6/ptodata/2/pubpna/US06_PUBCMB.seq:*

(cgn2_6/ptodata/2/pubpna/US06_PUBCMB.seq:*

(cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

(cgn2_6/ptodata/2/pubpna/US08_PUBCCMB.seq:*

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              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-401-000-4
US-10-401-000-3
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US-09-897-006-11
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Maximum Match 100%
Listing first 45 summaries
                                                                                   - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length
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Sequence 5, A
Sequence 5,
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Sequence 11
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Sequence 5,
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US-10-397-079-111
US-10-947-811-111
US-09-966-35-2-290
US-09-966-35-2-290
US-09-966-35-2-290
US-09-967-511A-4
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US-10-987-511A-5
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US-10-988-5-13
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US-10-988-5-13
US-10-988-5-13
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APPLICANT: Bremel, Robert D.
APPLICANT: Bleck, Gregory T.
APPLICANT: Indoden, Michael
APPLICANT: Eakle, Kurt
ITTLE OF INVENTION: Retrovirus-Based Genomic Scr.
FILE SPERENCE: GALA-07882
CURRENT APPLICATION NUMBER: US/10/397,569
CURRENT APPLICATION NUMBER: 60/368,396
PRIOR APPLICATION NUMBER: 60/368,396
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 1
LENGTH: 9009
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Sequence 1, Application US/09930377B Patent No. US20020144296A1
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98.3%;
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US-10-676-566-1
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1 ATGAIGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTGTT 60
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89.8%; Score 56.6; DB 18; Length 7490;
Best Local Similarity 93.7%; Pred. No. 6.1e-11;
Matches 59; Conservative 0; Mismatches 4; Indels 0;
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                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 93.7%;
Matches 59; Conservative
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LENGTH: 7472
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1 ATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTGTT 60
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                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wheeler, Matthew B.
APPLICANT: Wheeler, Barron M.
APPLICANT: Bleck, Gregory T.
APPLICANT: Bleck, Gregory T.
APPLICANT: Monaco-Seigel, Marcia
TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
FILE REFERENCE: 66-00
CURRENT APPLICATION NUMBER: US/09/930,377B
CURRENT FILING DATE: 2001-08-15
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 4532
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APPLICANT: Wheeler, Abaron M.
APPLICANT: Black, Sharon M.
APPLICANT: Black, Seigely Marcia
TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
FILE REFERENCE: 66-00A
CURRENT APPLICATION NUMBER: 08/10/676,566
CURRENT PILING DATE: 2003-09-30
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 4532
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ORGANIEM: Artificial Sequence
ORGANIEM: Artificial Sequence:alpha-LA/IGF-I
OTHER INFORMATION: gene construct
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Pred. No. 6.8e-11;
0; Mismatches 1;
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Best Local Similarity 98.3
Matches 57; Conservative
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APPLICANT: Bleck, Gregory
TITLE OF INVENTION: Expression Vectors
FILE REFERENCE: GALA-06415
CURRENT APPLICATION NUMBER: US/10/947,881
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                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Publication No. US20030224415A1
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, OTHER INFORMATION: Synthetic
US-10-759-315-11
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Sequence in Application US/09897511A
Fublication No. US2030092882A1
GENERAL INFORMATION:
APPLICANT: Bremel, Robert
APPLICANT: Miller, Linda
TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
FILE REFERENCE: GALA-06416
CURRENT FILING DATE: 2001-06-29
FRIOR PILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 5691
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100.0%; Pred. No. 9.9e-11;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                          Sequence 11, Application US/09897006

Patent No. US20020106729A1

GENERAL INFORMATION:
APPLICANT: Bleck, Gregory

TITLE OF INVENTION: Expression Vectors

FILE REPRENCE: GALA-06415

CURRENT APPLICATION NUMBER: US/09/897,006

CURRENT PILING DATE: 2001-06-29

PRIOR FILING DATE: 2000-07-03

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin Version 3.0

SEQ ID NO 11

LENGTH: 5691
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic
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Matches 56; Conservative
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US-09-897-511A-11
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US-10-397-079-11
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US-10-759-315-11
Sequence 11, Application US/10759315
Sequence 11, Application US/10759315
Sequence 11, Application US/040235173A1
Sequence 11, Application US/040235173A1
SERIAL INFORMATION:
APPLICANT: Bremel, Robert D.
APPLICANT: Miller, Linda U.
APPLICANT: Millor: Application of Host Cells Containing Multiple Integrating Vectors
TITLE OF INVENTION: by Serial Transduction
TITLE OF INVENTION: by Serial Transduction
CURRENT APPLICATION NUMBER: US/10/759,315
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.2
SEQ ID NO 11
LENGTH: 5691
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GENERAL INFORMATION:
APPLICANT: Bremel, Robert
APPLICANT: Miller, Linda
APPLICANT: Miller, Linda
APPLICANT: Miller, Linda
APPLICANT: Bleck, Gregory
TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
FILE REFERENCE: GALA-06419
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/897,511A
PRIOR APPLICATION NUMBER: 60/215,925
PRIOR APPLICATION NUMBER: 60/215,925
PRIOR PILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Version 3.0
SSEQ ID NO 11
LENGTH: 5691
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88.9%; Score 56; DB 17; L

Best Local Similarity 100.0%; Pred. No. 9.9e-11;

Matches 56; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 9.9e-11;
Matches 56; Conservative 0; Mismatches 0;
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2847 ATGCCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGAC 2906
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APPLICANT: Bremel, Robert
APPLICANT: Miller, Linda
APPLICANT: Bleck, Gregory
TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors; FILE REPERBNCE: GALA-06416; CURRENT PILING DATE: 2001-06-29; RIOR APPLICATION NUMBER: US/09/897,511A; CURRENT FILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 4207
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88.9%; Pred. No. 3.5e-09;
iive 0; Mismatches 7; Indels 0
                                                                                                                                                                                                            Query Match 87.3%; Score 55; DB 9; Length 284; Best Local Similarity 100.0%; Pred. No. 1.6e-10; Matches 55; Conservative 0; Mismatches 0; Indels
                                                                         TYPE: DNA
) ORGANISM: Bos taurus
) OTHER INFORMATION: Clone ID: 02-LIB2809-016-Q1-E1-A5
US-09-960-352-290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09897006; Patent No. US20020106729A1
GENERAL INFORMATION:
APPLICANT: Black, Gregory
TITLE OF INVENTION: Expression Vectors
FILE REFERENCE: GALA-06415; CURRENT APPLICATION NUMBER: US/09/897,006; CURRENT APPLICATION NUMBER: 60/215,851
PRIOR FILING DATE: 2000-07-03; NUMBER: OF SEQ ID NOS: 36; SOFTWARE: PatentIn version 3.0; SEQ ID NO 4
LENGTH: 4207
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ORGANISM: Artificial Sequence
FEATURE:
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     NUMBER OF SEQ ID NOS: 15112
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Matches 56; Conserv
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                             SEQ ID NO 290
LENGTH: 284
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Sequence 290, Application US/09960352
Batent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFRERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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Publication No. US20050100952A1

GENERAL INCORMATION:

APPLICANT: Bremel, Robert

APPLICANT: Miller, Linda

APPLICANT: Bleck, Gregory

TITLE OF INVENTION: HOST Cells Containing Multiple Integrating Vectors

FILE REFERENCE: GALA-06412-21

CURRENT APPLICATION NUMBER: US/11/018,895

CURRENT FILING DATE: 2004-12-21

PRIOR APPLICATION NUMBER: 05/29/887,511

PRIOR PRILING DATE: 2001-06-29

PRIOR PRILING DATE: 2000-03-30

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin version 3.0

SEQ ID NO 11

LENGTH: 5691
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100.0%; Pred. No. 9.9e-11;
iive 0; Mismatches 0; Indels (
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CURRENT FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: US/09/897,006
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/215,851
PRIOR FILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.0
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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LENGTH: 5691
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Sequence 4, Application US/10397079
Sequence 4, Application US/10397079
Sequence 4, Application No. US20030224415A1
GENERAL INFORMATION:
APPLICANT: Bremel, Robert
APPLICANT: Miller, Linda
APPLICANT: Miller, Linda
TITLE OF INVENTION: HOSE Cells Containing Multiple Integrating Vectors
FILE REFERENCE: CALA-06416
CURRENT APPLICATION NUMBER: US/09/9897,511A
PRIOR APPLICATION NUMBER: US/09/9897,511A
PRIOR APPLICATION NUMBER: 60/215,925
PRIOR APPLICATION NUMBER: 60/215,925
PRIOR PLING DATE: 2000-00-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
TYPE: DNA
TYPE: DNA
TYPE: DNA
CHARLES ARTIFICIAL SEQUENCE
FEATURE:
CHARLES ARTIFICIAL SEQUENCE
FEATURE:
CHARLES ARTIFICIAL SEQUENCE
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                                                                            Query Match 82.2%;
Best Local Similarity 88.9%;
Matches 56; Conservative
; OTHER INFORMATION: Synthetic US-09-897-511A-4
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Matches 56; Conservative
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BEVFKENINELSKDIGSESTEDQAMEAKQMKASSSSSEETTVPNSAFKTIQKEDVPS
ERYLGYLEQLLRLKKYNVPQLETVPNSAEEQLHSWKEGNPAHQKQPMIAVNQELAYFY
PQLFRQFYQLDAYPGGAWYYLDLGTQYTDAPGFSDINNFIGSBNSGKTTMPLW
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Peligini, M., Parma, P. and Vlaco, S. Peligini, M., Parma, P. and Vlaco, S. Direct Submission Submitted (17-JUL-2003) LEA- Laboratorio Epigenetica Applicata, Istituto Sperimenale Italiano 'Lazzaro Spallanzani', Via Giovanni XIII 7, Lodi, Lodi, Lodi 26900, Italy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Capra.
1 (bases 1 to 642)
U23157 Human pro-a
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/protein_id="AAR05658.1"
/db_xref="G1:37962703"
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AJ005430 Bubalus b
M33123 Bovine alph
AR26643 Sequence
M38641 Bovine mRNA
X72251 C.hircus mR
AJ504712 Capra hir
AJ504710 Capra hir
AJ504710 Capra hir
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AJ504710 Capra mr
AJ504710 Capra mr
AJ304713 Bos tauru
X63927 Sheep mRNA
X79327 Sheep mRNA
AK59836 C.hircus mR
AK002676 Sequence
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143703 Sequence
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Perfect score:
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Minimum DB Maximum DB

Database

Searched:

MAM 01-AUG-2004

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Gaps

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Result ģ us-10-820-777-2.rge

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Matches 39; Conserv
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AR266832
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SERYLGYLGYLEQLIRLKKYNVPQLEIVPNIABEQLHSMKEGIHAQQKEPMIGVNQELAYF
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                                                                                                                                                                                                                                                                                                                                                                       Das, P. Direct Submission Das P., National Institute of Immunology, Submitted (05-APR-1998) Das P., National Institute of Immunology, Gene Regulation Laboratory, Aruna Asaf Ali Marg, New Delhi- 110067,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (19-OCT-1998) Das P., National Institute of Immunology,
Gene Regulation Laboratory, Aruna Asaf Ali Marg, New Delhi- 110067,
                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bubalus.
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Bovine alpha-sl-casein mRNA, complete cds.
M33123
                                                                                                                               mRNA
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1. .645
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Bubalus bubalis mRNA for aS1-casein.
AJ005430
                                                                                                                                                                                                       Bubalus bubalis (water buffalo)
Bubalus bubalis
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polyA_site
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                    Agric. Biol. Chem. 48, 1663-1667 (1984)
Original source text: Bovine (strain Holstein) lactating mammary gland, cDNA to mRNA, clone p-alpha-s1 C228.
Location/Qualifiers
                                                                     1 (bases 1 to 1123)
Nagao,M., Maki,M., Sasaki,R. and Chiba,R.
Isolation and sequence analysis of bovine alpha-sl-casein CDNA
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109. .705
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ilarity 100.0%; Pred. No. 0.00033;
Conservative 0; Mismatches 0;
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64. .708
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Phenylalanine-free protein and DNA cc
Patent: US 6495344-A 40 17-DEC-2002;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAM 02-FEB-1995
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Caprinae, Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-MAY-1993) M. Jansa, Inst National de la Recherche Agronomique (INRA), Lab de Genetique Biochimique, INRA-CRJ 78350, Jouy-en-Josas, FRANCE Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perez,M.J., Leroux,C., Bonastre,A.S. and Martin,P. Occurrence of a LINE sequence in the 3' UTR of the goat alpha s1-casein E-encoding allele associated with reduced protein synthesis level
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                                                                                                                                                                                                                                                                                                                                               Length 1172;
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28. .672
                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ATGAAACTTCTCATCCTTACCTGTCTTGTGGGCTGTTGCT 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X72221.1 GI:311942
alpha-s1-casein; LINE element.
Capra hircus (goat)
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95011611
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                                                                                                                                                                                                                                                                             /citation=[1]
1150. .1155
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2 (bases 1 to 1554)
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 prim_transcript
old_sequence
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CHASICAS
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PEVGKKKVWELSKDIGSESTBOQAMBITKQMEABEISSSESTIVPNSYBOKHIQKEDVP
SERYLGYLEVLEQLLRLKKYKVPQLEIVPNSAEERLHSKKEGIDAQQKEPMIGVELAYF
YPELFRQFYQLLARYKYVPLGTQYTDAPSFSDIPNPIGSENSEKTTISLW"
   MAM 26-APR-1993
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                                                                                                                                                                   1 (bases 1 to 1134)
Gorodetskii,S.I., Zakhar'ev,V.M., Kyarshulite,D.R.,
Kapelinskaya,T.V. and Skryabin,K.G.
Cloning and nucleotide sequence of cDNA for bovine alpha-S1-casein
Blokhimia 51, 1402-1409 (1986)
Original source text: Bovine mammary gland, cDNA to mRNA.
Location/Qualifiers
                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Howkinse; Bos.

1 (bases 1 to 1172)

Stewart, A.F., Willis, I.M. and Mackinlay, A.G.

Stewart, A.F., Willis, I.M. and Mackinlay, A.G.

Nucleotide sequences of bovine alpha S1- and kappa-casein cDNAs

Nucleic Acids Res. 12 (9), 3895-3907 (1984)
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   linear
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Submitted (19-AUG-1986)
Data kindly reviewed (19-AUG-1986) by A. Stewart.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGAAACTICTCATCCTTACCTGTCTTGTGGCTGTTGCT 39
            Bovine alpha-S-1 casein mRNA, complete cds
M38641
 mRNA
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                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                  /product="alpha-S1-casein"
54. .708
                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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/protein_id="AAA30429.1"
/db_xref="G1:162794"
   1134 bp
                                                                                                                                                                                                                                                                                                               /organism="Bos taurus"
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/db_xref="taxon:9913"
7. _12
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Bos taurus (cow)
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                                                  M38641.1 GI:162793
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X00564.1 GI:175
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Bos taurus
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join(3416. .3466,5152. .5184,6067. .6105,6552. .6575,
6999. .7022,7610. .7633,8326. .8349,9863. .9894,10633. .10656,
10747. .10800,12149. .12167)
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                                                                                                                                                                                                                                                                                                                                                                                       3467. .5151
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/number=6
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3404. .3466
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7610. .7633
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7634. .8325
/gene="csn1S1"
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/number=8

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8350...9862

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/number=8
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/number=5
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                                                                                       /number=2
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                       'number=1
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5552...6575,6999...7022,7610...7633,8326...8349,9863...9894,

10633...10656,10747...10800,12149...12190,12834...12857,

14052...14093,15000...15026,15972...15995,16791...16945,

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YPQLFRQFYQLDAYPSGAWYYLPLGTQYTDAPSFSDIPNPIGSENSGKAAMPLW"
complement (839. .1296)
/note="Link element"
complement (859)
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/note="Link element"
/note="Link element"
/note="Link element"
/note="Link element"
                                                                                                                                                                                                                                                                                                                                                                                     CHISO4712 19406 bp DNA linear MAM 11-JUN-2003
Capra hircus csnlSl gene for alpha sl casein, allele N, exons 1-19.
AJS04712
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Caprinae, Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ramuno, L.
Direct Submission
Submitted (O2-UNN-2003) Ramuno L., Sc. zootecnica e Ispezione
Submitted (O2-UNN-2003) Ramuno L., Sc. zootecnica e Ispezione
Alimenti, Universita di Napoli Federico II, via Universita 133,
Portici (Na), Italia, 80055, ITALY
On Jun 12, 2003 this sequence version replaced gi:22796158.
Location/Qualifiers
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Direct Submission
Submitted (01-AUG-2002) Ramunno L., Sc. zootecnica e Ispezione
Alimenti, Universita di Napoli Federico II, via Universita 133,
Portici (Na), Italia, 80055, ITALY
revised by [3]
                                                                                                                                                                                                                                    Gaps
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Molecular characterization of the goat CSN1S1 N allele
                                                                                                                                                                                              78.0%; Score 39; DB 4; Length 1554; 100.0%; Pred. No. 0.00033; ive 0; Mismatches 0; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:9925"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                      AJ504712.2 GI:31620958
alpha sl casein; csn1Sl gene.
Capra hircus (goat)
Capra hircus
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2027. .3403
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Matches 39; Conserv
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Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Alimenti, Universita di Napoli Federico II, via Universita, 133,

Portici (Na), Italy, 80055, ITALY

Portici (Na), Italy, 80055, ITALY

On Jun 12, 2003 this sequence version replaced gi:22796154.

Location/Qualifiers

In: 19408

Application of Companisme Capra hircus

Application of Capra hircus

Applicatio
                                                                                                                                                                                                                                                                                                                                         CHISO4710 19408 bp DNA linear MAM 21-JUL-2004
Capra hircus csnlSl gene for alpha sl casein, allele A, exons 1-19.
AJ504710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ramunno,L., Cosenza,G., Rando,A., Illario,R., Gallo,D., Di
Berardino,D. and Masina,P.
The goat alphas1-casein gene: gene structure and promoter analysis
15256260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Caprinae, Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ramunno, L.
Direct Submission
Submitted (01-AUG-2002) Ramunno L., Sc. Zootecniche e Ispezione
Alimenti, Universita di Napoli Federico II, via Universita, 133,
Portici (Na), Italy, 80055, ITALY
revised by (3)
3 (bases I to 19408)
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alpha al casein; csnlSl gene.
Capra hircus (goat)
capra hircus
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Best Local Similarity
Matches 39; Conserv
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                        intron
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CHI504710
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JOURNAL
PUBMED
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JOURNAL
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REFERENCE
AUTHORS
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Capta hircus csn1S1 gene for alpha s1 casein, allele F, exons 1-19.
AJ504711 2 GI:31620956
alpha s1 casein; csn1S1 gene.
Capta hircus (goat)
                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Caprinae, Capra.
                                                                                                                                                                                                                                                                                                                                                                                        Ramunno, L.
Direct Submission
Submitted (01-AUG-2002) Ramunno L., Sc. Zootecniche e Ispezione
Alimenti, Universita di Napoli Federico II, via Universita 133,
Portici (Na), 80055 Italia, ITALY
revised by [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission

Submitted (02-UNN-2003) Ramunno L., Sc. Zootecniche e Ispezione
Alimenti, Universita di Napoli Federico II, via Universita 133,
Portici (Na), 80055 Italia, ITALY
On Jun 12, 2003 this sequence version replaced gi:22796156.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            function="important role in the capacity of milk to ransport calcium phosphate" codon_start=1
                                                                                                                                                                                                                                                                                                                      {\tt Ramunno,L.} \\ {\tt Molecular} \ \ {\tt characterization} \ \  {\tt of} \ \ {\tt the} \ \ {\tt goat} \ \ {\tt CSNISI} \ \ {\tt F} \ \ {\tt allele} \\ {\tt Unpublished} \\
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                     MAM 24-OCT-1991
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Submitted (28-MAY-1991) D. Koczan, Inst f Mikro- und,
Molekularbiologie / JLU, Frankfurterstr. 107, 6300 Giessen, FRG
For related sequences see Stewart A.F., NAR 12:3895-3907(1984) and
Yu-Lee L., NAR 14:1883-1902(1986).
Location/Qualifiers
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Koczan, D., Hobom, G. and Seyfert, H.M.

Genomic organization of the bovine alpha-S1 casein gene

Nucleic Acids Res. 19 (20), 5591-5596 (1991)
                     linear
                                                                                                                         alpha-s1-casein; milk protein; phosphoprotein.
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                  22069 bp B.taurus gene for alpha-S1-casein.
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WURNY, D.M. Adama, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabrooks, S.L., Amaretunge, H.C., Are, J.R., Ayele, M. Benks, T., Babbrooks, S.L., Amaretunge, H.C., Are, J.R., Ayele, M. Benks, T., Babbrooks, S.L., Briton, J. Bimage, K., Blankenburg, K., Bonnin, D., Budbrooks, S.L., Briton, H. Brown, E., Brown, M., Bryant, N.P., Buday, C., Burch, P., Burkett, C., Burchl, K.L., Dray, J. M. Carron, T. Carron, T. Carron, T. Carron, T. Carron, C., Chen, R., Chen, R., Chen, R., Chen, R., Chen, R., Chen, R., Chen, C., Chen, R., Chen, C., Coyle, M. D. Dathorne, S.R., David, R., Davis, C., Davy-Carroll, L., Dedrich, D. A., Delaney, K.R., Darger, H. Dugan-Rocha, S., Dutbin, K.J., Barnhart, C., Edgar, D., Edwarde, C.C., Elbaj, C., Escotto, M., Falla, M., Dugar, Rocha, S., Dutbin, K.J., Barnhart, C., Edgar, D., Edwarde, C.C., Elbaj, C., Escotto, M., Goria, A., Garner, T., Garza, N., Gill, K., Gorrell, J.H., Gover, C., Hollins, B., Hernandez, O., Hodgson, M., Hogues, M., Holloway, C., Hollins, B., Hernandez, C., Hartis, K., Hark, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, M., Hogues, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Johlivet, S., Joudah, S., Joudah, S., Jouch, M., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louleeged, H., Lozado, R.G., Lu, W., Leal, B., Martin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Massey, B., Martin, R., Marcin, M., Mayuen, M., Mouven, G., Miner, C., Minch, M., Mayuen, M., Mouven, G., Miner, C., Minch, M., Mayue, M., Morris, S., Savery, G., Scherer, S., Soott, G., Mang, P., Peters, L., Velle, M., Nickerson, E., Wanken, M., Stocher, S., Soott, G., Mang, S., Oqui, M., Stocher, S., Soott, G., Marcin, R., Washington, C., Wang, S., Wall, M., Yer, Wu, Y., Wu, Y. F., Tangeris, A., Tangeris, A., Tangeris, A., Tangeris, A., Tangeris, A., Tangeris, A., Marin, G., Wallilanson, A., Wallianson, A., Walled, D., Wallianson, A., Walled, D., Wallianson, A., Walled, D., Wall, M., Walled, D., Wall, M., Walled, D., W
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Direct Submission
Submitted (24.5EP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 195534)
Worley, K.C.
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Submitted (27-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Genome Center
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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Best Local Similarity 100.
Matches 39; Conservative
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> AC134173 195534 bp DNA linear HTG 27-SEP-2002 Bos taurus clone RP42-254113, WORKING DRAFT SEQUENCE, 26 unordered pieces.

LOCUS DEFINITION

RESULT 12 AC134173

8 6

AC134173 AC134173.1 GI:23306007 HTG, HTGS_PHASE1; HTGS_DRAFT. Bos taurus (Cow)

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE

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sig_peptide
mat_peptide
        Query Match
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AUTHORS
TITLE
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MEDLINE
PUBMED
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                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Consensus quality: 192466 bases at least Q20
Estimated insert size: 204493; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                          2358: contig of 2358 bp in length 2458: gap of unknown length 5719: contig of 3161 bp in length 8310: contig of 2591 bp in length 8310: contig of 2591 bp in length 1102: contig of 2592 bp in length 1102: contig of 2592 bp in length 11486: contig of 3284 bp in length 14466: gap of unknown length 1749: contig of 2663 bp in length 1744: contig of 2664 bp in length 1744: contig of 
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21514: gap of unknown length
25271: contig of 3657 bp in length
30552: contig of 5374 bp in length
30745: gap of unknown length
30745: gap of unknown length
36182: contig of 5437 bp in length
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195534: contig of 29020 bp in length.
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116816: gap of unknown length
128293: contig of 11477 bp in length
128393: gap of unknown length
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87761: contig of 7631 bp in length
87861: gap of unknown length
95726: contig of 7865 bp in length
95826: gap of unknown length
95836: gap of unknown length
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105054: contig of 9228 bp in length
105154: gap of unknown length
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138140: contig of 9747 bp in length
138240: gap of unknown length
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of 5674 bp in length
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of 6038 bp in length
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/db_xref="taxon:9913"
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/clone="RP42-254113"

ORIGIN

FEATURES

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.

1 (bases 1 to 1110)

Mercier, J.C., Gaye, P., Soulier, S., Hue-Delahaie, D. and Vilotte, J.L. Construction and identification of recombinant plasmids carrying construction and identification of recombinant plasmids carrying and beta-lactoglobulin. Nucleotide sequence of alpha S1-casein Biochimie 67 (9), 959-971 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MKLLILTCLVAVALARPKHPIKHQGLSPEVLNENLLRFVVAPFP
PERKENIPRELKDIGSES IEDQAMBACKOMKAGSSSSSERITYPNSAEQKYIQKEDVP
SERYLGYLEQLLALKKYNYPQLEIYPKSAEEQLHSKKEGNPHHQKQPYANQLFRQF
YQLDAYPSGAWYYLPLGTQYTDAPSFSDIPNPIGSENSGKITMPLW"
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Location/Qualifiers
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/protein_id="CAA26982.1"
/db_xref="G1:1248"
/db_xref="UniProt/Swiss-Prot:P04653"
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52. .682
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Pred. No. 0.00081;
0; Mismatches 1;
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            DB 2;
78.0%; Score ... 000v
100.0%; Pred. No. 0.0vv
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/product="alpha-S1-casein"
1088. .1093
                                                                                                                                                                                                                     OACSASIR 1110 bp
Sheep mRNA for alpha-S1-casein.
X03237
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/db_xref="taxon:9940"
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Capra hircus (goat)
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Best Local Similarity 97.4%;
Matches 38; Conservative (
                                                                                                                                                                                                                                                                                                                              Ovis aries (sheep)
Ovis aries
                                                   39; Conservative
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polyA_site
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ACCESSION
VERSION
KEYWORDS
SOURCE
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/ Godon start=1
/ Codon start=1
/ Drotein id="CA42496.1"
/ Drotein id="
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1 (bases 1 to 51)
1 (bases 1 to 51)
Debber, H. A., Strijker, R., Heyneker, H.L., Platenburg, G., Lee, S.He., Pieper, F. an Krimpenfort, P.J.A.
Transgenic bovine
Patent: US 5741957-A 37 21-APR-1998;
Location/Qualifiers
                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Caprinae, Capra.
                                                                                                                                                                                                                                                                                                                                                                                                         Martin,P.
Direct Submission
Submitted (27-MAY-1991) P. Martin, Lab. de Genetique biochimique,
INRA, 78352 Jouy-en-Josas, France
Location/Qualifiers
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                                                                                                    l (bases lformand Martin, P. Leroux, C., Mazure, N. and Martin, P. Mutations away from splice site recognition sequences might cis-modulate alternative splicing of goat alpha sl-casein transcripts. Structural organization of the relevant gene 92210588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="mammary gland"
/clone_lib="pUC18/Smal wcDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AR002676 51 bp | Sequence 37 from patent US 5741957.
AR002676 GI:3964230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Capra hircus"
/mol_type="mRNA"
/db_xref="taxon:9925"
/clone="as1-Cn A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="asl-casein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="as1-casein"
/note="cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="as1-casein"
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Best Local Similarity
Capra hircus
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DEFINITION
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JOURNAL
FEATURES
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
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Search completed: October 1, 2005, 14:10:04 Job time : 860.407 secs

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Abx35576 Bovine ES Abx46229 Bovine ES Aaq14051 Rennin ge Aaq14050 Alpha-SI-Abx39403 Bovine ES Abx35508 Bovine ES Abx35508 Bovine ES Abx35508 Bovine ES Abx36508 Tovine ES Aax69774 Bovine ES Aax69741 Linker GP Aax6974 Transgeni Aaq67694 Transgeni Aaq67694 Transgeni Aaq7695 Bovine ES Abx37508 Bovine ES Abx37209 Bovine ES Aach313166 Human ste Abx37209 Bovine ES Aach37209 Bovine ES

ABX46229
AARX35247
AAQ14051
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Aaqu6046 Probe 2 t
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Abx4768 Bovine ES
Abx35788 Bovine ES
Abx43873 Bovine ES
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Abx4977 Bovine ES
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Abx48129 Bovine ES
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Abx4741 Bovine ES
Abx4741 Bovine ES
Abx48129 Bovine ES
Abx3818 Bovine ES
Abx36129 Bovine ES
                                                                 ; Search time 296.018 Seconds (without alignments) 999.897 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                        1 atgaaacttctcatccttac.....gctgttgctgccaggttaac
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                 4390206 seqs, 2959870667 residues
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                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  October 1, 2005, 11:36:51
                                            nucleic search, using sw model
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AAQ14774
AAQ14774
ABX35784
ABX35788
ABX45526
ABX45526
ABX49077
ABX49077
ABX49677
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Gapop 10.0 , Gapext 1.0
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No.
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ALIGNMENTS

AAQ06046	
	AAQ06046 standard; DNA; 40 BP.
AL AMOUN	AACOOUSO;
	26 - MAD - 2002 (*********************************
DE Probe	be 2 to signal sequence of alpha S1 casein Chromosomal
××)
	Bovine alpha S1 casein chromosomal gene; transgenic mice;
XX OS Synth	Synthetic
	EP390592-A.
אא הייים הפ	03-0CT-1990
	30-MAR-1990; 90EP-00303445.
XX	
	31-MAK-1989; 6908-000/63/4.
PA (KYOW)	OW) KYOWA HAKKO KOGYO KK.
PI Sekine	ine S, Ito S, Katsuki M;
	WPI; 1990-299492/40.
	ina
	transgenic animals using promoter of bovine alpha S1 casein chromosomal
PT gene.	ů
PS Examp	Example; Page 7; 55pp; English.
	High molecular weight DNA from bovine liver was partially digested by
	Sau3A and inserted into EMBL3 vector. Plaques were screened with two
	probes (#1 and #2). Probe 1 corresponds to the 5' non- coding region
	bovine alpha S1 casein cDNA and a part of exon 1 of alpha S1 савеin
CC chrom	chromosomal gene. Probe 2 corresponds to part of the signal sequence

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The constructs provide high yields of the protein with simple recovery from the milk. Activation of the gene occurs only in the mammary gland. See also AAQ14050-51, AAQ14774-77. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant DNA constructs for expressing protein in milk - contg. specific mammary gland transcription control region and signal sequence, providing high yield and easy prod. recovery.
                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/note= "derived from alpha-S1-casein gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 78.0%; Score 39; DB 2; Length 303
Local Similarity 100.0%; Pred. No. 9e-05;
Les 39; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 303 BP; 45 A; 109 C; 90 G; 59 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGAAACTICICATCCTTACCTGTCTTGTGGCTGTTGCT 39
     14 ATGAAACTICTCATCCTTACCTGTCTTGTGGCTGTTGCT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT
                                                                                                                                                                                                                                                      Alpha-S1-casein gene; mammary gland; IGF-I; ss.
                                                                                                                                                                                                                   IGF-I under alpha-S1-casein control regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/note= "3' casein domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3 (d); Page 11; 41pp; German
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CONE ) CONSORTIUM ELEKTROCHEM IND
                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                           59. .271
/*tag= b
/label= IGF-I
272. .303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91EP-00105702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90DE-04011751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90DE-04012526
                                                                                             AAQ14776 standard; DNA; 303
                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-304858/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brem G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-1990;
                                                                                                                                                                25-MAR-2003
06-JAN-1992
                                                                                                                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP451823-A.
                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                               AAQ14776;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
                                                        RESULT 3
AAQ14776
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from screening 150000 plaques. The promoter was then isolated from the gene. See also Q06045, Q06047-Q06049 and Q06392. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant DNA constructs for expressing protein in milk - contg. specific mammary gland transcription control region and signal sequence, providing high yield and easy prod. recovery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The rennin gene was ligated to the alpha-S1-casein promoter using the signal peptide sequence of the alpha-S1-casein gene. The constructs provide high yields of the protein with simple recovery from the milk. Activation of the gene occurs only in the mammary gland. See also AAQ14050-51, AAQ14774-77. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
                                                                                                         78.0%; Score 39; DB 2; Length 40; 100.0%; Pred. No. 5.9e-05; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/label= alpha-S1-casein-signal_peptide
59. .77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 82 BP; 17 A; 24 C; 16 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGAAACTTCTCATCCTTACCTGTCTGTGGCTGTTGCT 39
                                                                                                                                                                                 39
                                                                                                                                                                                                   1 ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT 39
                                                                         Sequence 40 BP; 6 A; 11 C; 7 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prorennin; alpha-S1-casein gene; mammary gland; ss.
                                                                                                                                                                                 1 ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3 (b); Page 9; 41pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/label= prorennin
                                                                                                                                                                                                                                                                                                         BP
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                                                                                                                                                                                                                                                                                                       AAQ14774 standard; DNA; 82
                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                    Query Match
Best Local Similarity 100.0
Matches 39, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-304858/42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
06-JAN-1992
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19-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP451823-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                          AAQ14774;
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Gaps

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52

21-FEB-2003

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Length 303;

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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically phybridise to a second nucleic acid molecule comprising any of 1512 nuclectide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are if (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or issue comprising; (a) incubating a marker nucleic acid (comprising any complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or issue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is predictive of the level or pattern of the complementary nucleic acid is used for the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                              Bovine, ss; EST; expressed sequence tag; lactation; LMFD;
muscle deposition; fat deposition; genome mapping; gene identification;
gene analysis; cattle breeding.
                    Bovine EST associated with lactation/muscle/fat deposition #12853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         segdata.uspto.gov/seguence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; SEQ ID NO 12853; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tao N,
                                                                                                                                                                                                                                                                                                                                  12-JAN-1999; 99US-0115707P,
11-JAN-2000; 2000US-00480902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mathialagan N,
                                                                                                                                                                                                                                                                                                                                                                                                                        MATHIALAGAN N.
TAO N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-110599/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAON/) TAO N.
(WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                   BYAT/) BYATT J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    format
                                                                                                                                                                                              US2002137139-A1.
                                                                                                                                                                                                                                            26-SEP-2002,
                                                                                                                                                      Bos Taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Byatt JC,
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Gaps
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                          Length 337;
                                                    0; Indels
Sequence 337 BP; 83 A; 68 C; 77 G; 108 T; 0 U; 1 Other;
                          Score 39; DB 8; I
Pred. No. 9.2e-05;
                 78.0%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
              Query Match
Best Local Similarity 100.0
....hes 39; Conservative
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RESULT 5 ABX35788/c

g 8

The invention relates to a purified nucleic acid molecule associated with cattation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can appecifically hybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences, appearing as ABX34836-ABX49347, or complements of them. Also included are cid il a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that thurstions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and cid polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and cid secremining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid sequences of the molecule of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is used for determining a level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapphing, gene identification and analysis, cattle correction of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the constructs for use in cattle gene expression, or constructs and analysis, and the constructs and analysis, and the constructs are sequence tag) nucleic acid in the constructs and analysis, and include the constructs and analysis, and the constructs are constructed to the processor sequence tag) nucleic acid in the constructs of th New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle. Bovine; 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding. 3ovine EST associated with lactation/muscle/fat deposition #953. Tao N, Warren WC; Claim 2; SEQ ID NO 953; 245pp; English. ABX35788 standard; cDNA; 375 BP. 24-SEP-2001; 2001US-00960352. 12-JAN-1999; 99US-0115707P. (first entry) 3yatt JC, Mathialagan N, (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N. WPI; 2003-110599/10. (WARR/) WARREN W C. JS2002137139-A1 TAO N 20-FEB-2003 26-SEP-2002. 30s Taurus. ABX35788; (TAON/

1 ATGAAACTICICAICCTIACCTGICTIGIGGCTGIIGCT 100.0%; Prea. ...

à

Conservative

Query Match Best Local Similarity Matches 39; Conserv

present sequence was not shown in the specification but was obtained in

electronic format from the USPTO web site: segdata.uspto.gov/sequence.html?DocID=20020137139

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Gaps

.. 0

Length 375; 0; Indels

78.0%; Score 39; DB 8; Le 100.0%; Pred. No. 9.4e-05;

Sequence 375 BP; 97 A; 85 C; 77 G; 116 T; 0 U; 0 Other;

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368 ATGAAACTICTCATCCTTACCTGTCTTGTGGCTGTTGCT 330

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New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                       Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bovine LMFD \overline{B}ST (expressed sequence tag) nucleic acids. Note: The nt sequence was not shown in the specification but was obtained in
                                                                       Bovine EST associated with lactation/muscle/fat deposition #10691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 388 BP; 113 A; 80 C; 91 G; 104 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      segdata.uspto.gov/seguence.html?DocID=20020137139
                                                                                                                                                                                                                                                                             Tao N, Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 10691; 245pp; English.
                  ABX45526 standard; cDNA; 388 BP
                                                                                                                                                                                    24-SEP-2001; 2001US-00960352.
                                                                                                                                                                                                     12-JAN-1999; 99US-0115707P,
11-JAN-2000; 2000US-00480902.
                                                                                                                                                                                                                                                                             Mathialagan N,
                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence was not
                                                                                                                                                                                                                               (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
(TAON/) TAO N.
(WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                WPI; 2003-110599/10.
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                                                     21-FEB-2003
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                                                                                                                              Bos Taurus.
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                                    ABX45526;
         ABX4552
RESULT
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The invention relates to a purified mucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMPD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bowine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule betained from the bowine cell or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                               Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                Gaps
                                                                                                                                                                                                                                                     Bovine EST associated with lactation/muscle/fat deposition #9038.
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              Indels
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                                                                          54 Argaacricicarccriaccrercricicaccreriscr 92
Pred. No. 9.5e-05;
Mismatches 0;
                                              1 ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT
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                Mismatches
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                                                                                                                                                        ABX43873 standard; cDNA; 394 BP
100.08;
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11-JAN-2000; 2000US-00480902.
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                                                                                                                                                                                                                       21-FEB-2003 (first entry)
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                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BYAT/) BYATT J C. (MATH/) MATHIALAGAN
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WARREN W C.
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2002
                  39;
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                                                                                                                                                                                         ABX43873;
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(TAON/)
                Matches
                                                                                                                                            ABX43873/
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The useful for genome mapping, gene identification and analysis, cattle
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                                                                                                                                                                                                                                                                                                                       Bovine, 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                    Gaps
                                                                                                                                                                                                                                                                                             Bovine EST associated with lactation/muscle/fat deposition #14946
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                                                     78.0%; Score 39; DB 8; Length 394; 100.0%; Pred. No. 9.5e-05; ive 0; Mismatches 0; Indels
                             Sequence 394 BP; 109 A; 92 C; 82 G; 111 T; 0 U; 0 Other;
                                                                                                                             341 ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT 303
                                                                                                             1 ATGAAACTICTCATCCTTACCTGTCTTGTGGCTGTTGCT 39
segdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Byatt JC, Mathialagan N, Tao N, Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 14946; 245pp; English.
                                                                                                                                                                                                          ABX49781 standard; cDNA; 399 BP.
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                                                                                                                                                                                                                                                                   (first entry)
                                        Query Match
Best Local Similarity 100...
These 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
(TAON/) TAO N.
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                                                                                                                                                                                                                                                                                                                                                                                                            US2002137139-A1.
                                                                                                                                                                                                                                                                   21-FEB-2003
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid another acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nuclectide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are if (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that cuctions in the cell to cause termination of transcription and addition of polyadenylated ribonuclectides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b)
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breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMPD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?DocID=20020137139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine; 88; BST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                 Length 399;
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                                                                                                                                                                                                                                                                       Sequence 399 BP; 107 A; 93 C; 83 G; 116 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39
                                                                                                                                                                                                                                                                                                                                             'Match 78.0%; Score 39; DB 8; Le Local Similarity 100.0%; Pred. No. 9.5e-05; les 39; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGAAACTICTCATCCTTACCTGTCTTGTGGCTGTTGCT
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11-JAN-2000; 2000US-00480902.
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                                                                                                                                                                                                                                                                                                                                             Query Match
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(WARR/)
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(a) incubating a marker nucleic acid (comprising any

tissue comprising:

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               the detection of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 1512 bowine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are i(1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or
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 detecting the level or pattern of the complementary nucleic acid, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed sequence tag; lactation; LMFD; 1; fat deposition; genome mapping; gene identification;
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                                                                                                                                                                                                                                                               Score 39; DB 8; Length 408;
Pred. No. 9.6e-05;
                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                          Sequence 408 BP; 109 A; 93 C; 85 G; 121 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                 ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT 324
                                                                                                                                                                                                                                                                                                                                          1 ATGAAACTICICATCCTTACCTGTCTTGTGGCTGTTGCT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tao N, Warren WC;
                                                                                                                                                                                                                                                                           100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABX49077 standard; cDNA; 408 BP
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                                                                                                                                                                                                                                                                 78.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-110599/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine; ss; EST; e)
muscle deposition;
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                                                                complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is predictive of the level or pattern of the complementary nucleic acid is predictive of the detection of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine call or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are
            of the 15112 nucleic acid sequences or its complement or fragment) with complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
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                                                                                                                                                                                                                                                                                                                          Sequence 408 BP; 105 A; 88 C; 80 G; 135 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT 289
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9.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABX44547 standard; cDNA; 411 BP
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gene analysis; cattle breeding.
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11-JAN-2000; 2000US-00480902.
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Best Local Similarity 100.
Matches 39; Conservative
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acid linked to a promoter and a 3' non- translated sequence that
functions in the cell to cause termination of transcription and addition
of polyademylated ribonucleotides to a 3' end of the mRNA molecule; and
tissue comprising.

(2) determining a level or pattern of a molecule in a bovine cell or
tissue comprising.
(3) incubating a marker nucleic acid (comprising any
of the 15112 nucleic acid molecule obtained from the bovine cell or
tissue, where hybridisation between the marker nucleic acid and the
complementary nucleic acid molecule obtained from the bovine cell or
tissue, where hybridisation between the marker nucleic acid, where
the complementary nucleic acid permits the detection of the molecule; and
detecting the level or pattern of the complementary nucleic acid, where
the detection of the complementary nucleic acid is predictive of the
level or pattern of the molecule. The LMFD nucleic acid is used for
determining a level or pattern of a molecule in a bovine cell or tissue.
It is useful for genome mapping, gene identification and analysis, cattle
breeding, preparation of constructs for use in cattle gene expression, or
for genetically improving cattle. The present sequence is one of the
present sequence was not shown in the specification but was obtained in
electronic format from the upper or side.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 411 BP; 88 A; 117 C; 102 G; 104 T; 0 U; 0 Other;
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Pred. No. 9.6e-05;
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'.ve 0; Mismatches
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ABX47441 standard; cDNA; 412 BP
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(MATH/) MATHIALAGAN N.
(TAON/) TAO N.
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Best Local Similarity
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The invention relates to a purified mucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from a cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences.

C anid linked to a promoter and a 3' non- translated sequence that the call to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating amarker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement earl or transcription of transcription and addition of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid permits the detection of the molecule, and the complementary nucleic acid permits the detection of the molecule, and the complementary nucleic acid permits the detection of the molecule, and the complementary nucleic acid sequences or its complementary nucleic acid sequence to the complementary nucleic acid sequence or complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is used for the determining a level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of energiance is one of the complementary nucleic acid is predictive or breading, preparation of constructs for use in cattle gene expression, or breading preparation of expression in the molecule or pattern or pattern of the molecule or in cattle gene expression, or breading preparation of expression in the molecule or pattern or pattern or in cattle gene expression, or breading provine unit in the pres
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11-JAN-2000; 2000US-00480902.
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Matches 39; Conservative
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MATHIALAGAN
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(WARR/) WARREN W C.
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ABX39376/c
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically Mybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences.

The invention as ABX34836-ABX49947, or complements of them. Also included are complemented as a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of functions in the cell to cause termination of transcription and addition of complementary nucleic acid sequences to a 3' end of the mRNA molecule; and to the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the molecule; and the complementary nucleic acid molecule of the complementary nucleic acid molecule of the complementary nucleic acid, where the detection of the molecule. The LMFD nucleic acid is predictive of the complementary nucleic acid, sused for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for geneme mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the present sequence is one of the present sequence and an analysis, and in the present sequence and and analysis.
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deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence was not shown in the specification but was obtained in
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segdata.uspto.gov/sequence.html?DocID=20020137139
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                                                            Claim 2; SEQ ID NO 4541; 245pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BYATT J C.
MATHIALAGAN N.
TAO N.
WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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(TAON/)
(WARR/)
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences, appearing as ABX34836-ABX4947, or complements of them. Also included are i. (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule acid (comprising any of the 15112 nucleic acid sequences or its complement ell or runcleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or involvation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule, and (b) detecting the level or pattern of the complementary nucleic acid sequence cell or tissue. The detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for the genetically improving cattle. The present sequence is one of the complement sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:

"Sequence of the complement of the sequence tages of acides of acides of a sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                 New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : ss; EST; expressed sequence tag; lactation; LMFD; deposition; fat deposition; genome mapping; gene identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine EST associated with lactation/muscle/fat deposition #13294.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 92 c, ...
78.0%; Score 39; DB 8; Lengtu ...
78.0%; Pred, No. 9.6e-05; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 417 BP; 111 A; 92 C; 89 G; 125 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 Argaaacricicarccriaccrercrisisesereriscr 324
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    Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 100.0%; Pred. No. 9.6
Conservative 0; Mismatches
                                                                                                                                                                       Claim 2; SEQ ID NO 13070; 245pp; English.
    Tao N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABX48129 standard; cDNA; 428
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11-JAN-2000; 2000US-00480902.
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Byatt JC, Mathialagan N,
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                                         WPI; 2003-110599/10.
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Les 39; Conserv
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Query Match

Best Local Similarity 100.0%; Score 39; DB 8; Length 428;

Matches 39; Conservative 0; Mismatches 0; Indels

1 ATGAACTTCTCATCCTTACCTGTGGGTGTTGCT 39

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0; Gaps

Db 185 ATGAACTICTCATCCTTACCTGTCTTGTGGCTGTTGCT 223

Search completed: October 1, 2005, 13:37:32 Job time : 298.018 secs

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Searched:

Minimum Maximum Database

Result ģ

Sequence: Title: Perfect (

Run on:

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Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRimmerch 12 options.
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Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 357)
Sonstegard,T., Capuco,A.V., White,J., Van Tassell,C.P.,
Sonstegard,T., Capuco,A.V., White,J., Van Tassell,C.P.,
Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
Analyais of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG692772 342586 BARC 5BOV BOS taurus cDNA 5', mRNA sequence
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Plate: 43 row: C column: 3
Seg primer: ATTTAGGTGACACTATAG.
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                                                                                                                                     (without alignments)
820.069 Million cell updates/sec
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               GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                               nucleic search, using sw model
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                                                                               nucleic
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EST 27-MAR-2003

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Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                   Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index Mamm. Genome 13 (7), 373-379 (2002) 22135956
                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                           1 (bases 1 to 105)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Comnor, B. B., Cho, J., Sultana, R., Shade, L., Wray, J.B., Wells, K.D.
and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                        Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
USDA, ARS, Beltsville Agricultural Research Center
USDA, ARS, Beltsville, MD 20705, USA
Tel: 301 504 8414
Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 141 row: O column: 16
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG
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PCR PRimers
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BE477105.1 GI:9596575
                    BE479124.1 GI:9598657
                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                           Bos taurus (cow)
                                                                                                                                        Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                            12140684
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                                                                                ORGANISM
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PUBMED
COMMENT
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                                                                                                                                                                                 AUTHORS
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BE477105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USDA, ARS, Beltsville Agricultural Research Center
Balg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8416
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRimers
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//note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease states."
                                                                                                                                                                                                                                                              EST 27-MAR-2003
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Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.B., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
Analysis of bovine mammary gland EST and functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                  Gaps
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                               78.0%; Score 39; DB 2; Length 103; 100.0%; Pred. No. 0.0037; ive 0; Mismatches 0; Indels
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                                                                                                                 1 ATGAAACTICICAICCTTACCTGICTIGIGGCIGITGCIG 40
                                                                                                                                        ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCTG 91
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                                                         l Similarity 100.0%; Pred. No. 0.0 40; Conservative 0; Mismatches
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Mamm. Genome 13 (7), 373-379 (2002)
22135956
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BACKWARD: GTTTCCCAGTCACGACG
Plate: 113 row: B column: 6
Seg primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                    BE845866.1 GI:10282690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Sonstegard TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                   Query Match
Best Local Similarity
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les 39; Conserv
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BE845866
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/tissue_type="pooled"
/lab host="DH108"
/clone lib="BHC 5BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
/library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
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1 (bases 1 to 108)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
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160562 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                   Query Match 78.0%; Score 39; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 39; Conservative 0; Mismatches
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Email: tade@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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/db_xref="taxon:9913"
/tisue_type="mooled"
/lab_host="barc spow"
/clone_lib="BARC 5BOV"
/note="Vector: pCNV 9PORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
                                                                                        /mol_type="mRNA"
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//db xref="taxon:9913"
//idsue_type="pooled"
/lab host="DHC 5BOV"
//clone lib="BARC 5BOV"
//clone lib="BARC 5BOV"
//clone lib="Roctor: pCNV 5PORT6; Site_1: Not1; Site_2: Sal1;
//clone lib="rector: pCNV 5PORT6; Site_1: Not1; Site_2: Sal1;
//clone lib="ade from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 113)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
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                                                                                                                                                                                                                                                                                                                                                       Length 110;
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USDA, ARS, Beltsville Agricultural Research Center
USDA, ARS, Beltsville, MD 20705, USA
Tel: 301 504 8414
Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BES89286 113 bp mRNA linear
195358 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
BES89286
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/organism="Bos taurus"
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Seg primer: ATTTAGGTGACACTATAG.
Seq primer: ATTTAGGTGACACTATAG
                          Location/Qualifiers
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nes 39; Conserv
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COMMENT
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KEYWORDS
SOURCE
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BE589286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                    Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
USDA, ARS, Beltsville Agricultural Research Center
Bd1g. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Rax: 301 504 8416
Bmail: tads@lpgai.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCAGATAGACG
BACKWARD: GTTTAGGTGACACTATAG.
Seq primer: ATTTAGGTGACACTATAG.
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="BARC 5BOV"
hote="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sonsiegard, T., Capuco, A.V., White, J., Van Tassell, C.P., Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D. and Quackenbush, J. Sultana, R., Shade, L., Wray, J.E., Wells, K.D. Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index ammum. Genome 13 (7), 373-379 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 108;
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Fax: 301 504 8414
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24 AIGAAACTICTCAICCTTACCIGICTIGIGGCIGTIGCT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 78.0%; Score 39; DB 2; I Best Local Similarity 100.0%; Pred. No. 0.0037; Matches 39; Conservative 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 110)
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Matches

ò 셤 SOURCE ORGANISM

RESULT 7 BE481164

REFERENCE AUTHORS JOURNAL MEDLINE PUBMED

COMMENT

TITLE

FEATURES

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Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8414
Email: tadaselps: barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="pooled"
/lab_host="DH10B"
/clone_llb="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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                                                                                                                  1 (Dases 1 to 119)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Sonort, E.B., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 130)
Sonstegard,T., Capuco,A.V., White,J., Van Tassell,C.P.,
Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
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o, 0.0038;
0; Indels
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20 ATGAAACTICTCATCCTTACCTGTCTTGTGGCTGTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.0%; Score 39; DB ilarity 100.0%; Pred. No. 0.0 Conservative 0; Mismatches
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 31 row: B column: 1
Seq primer: ATTTAGGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9913"
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PCR PRimers
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                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovinae; Bos.
                          Bos taurus (cow)
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Best Local Similarity
Matches 39; Conserv
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BE486332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: tadsolpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
VO.990904-e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PORR PRIMERS
FORWARD: AGGAAACGCTATGACCAT
BACKWARD: GTTTTCCCAGTCAGGACG
Plate: 9 row: D column: 5
Seq primer: ATTTAGGTGACATTAGG.

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/lab_host="DH108"
/clone_lib="BARC_5BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made_from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 114)
Sonstegard, T. Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E. B., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
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    Score 39; DB 2; Length 113;
Pred. No. 0.0038;
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166493 BARC 5BOV Bos taurus CDNA 5', mRNA sequence.
BE481164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contract: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
TH: 301 504 8414
Fax: 301 504 8414
                                              0; Indels
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                                                                                        1 ATGAAACTICTCATCCTTACCTGTCTTGTGGCTGTTGCT
                                                                                                              ATGAAACTICICATCCTTACCTGTCTTGTGGCTGTTGCT
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/db_xref="taxon:9913"
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    78.0%;
                                              39; Conservative
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Bos taurus
Query Match
Best Local Similarity
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Best Local S:
Matches 39,
                                                                                                                                                                                                                                                    DEFINITION
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EST 27-MAR-2003

RESULT 8 BG694048 LOCUS

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Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                 /clone_lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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/folone lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
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Mamm. Genome 13 (7), 373-379 (2002)
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases I to 132)
Sonstegard,T., Capuco,A.V., White,J., Van Tassell,C.P.,
Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
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BG690967
                                                                                                                                                                                                                                                                                               Length 132;
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USDA, ARS, Beltsville Agricultural Research Center
Bd1g. 200 Rm 2A, Beltsville, MD 20705, USA
Bd1s. 301 504 Bd16
Fax: 301 504 B414
Email: tads@lpsi.barc.usda.gov
                                                                                                                                                                                                                                                                                                                                           0; Indels
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Pred. No. 0.0039;
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100.0%; Pred. No. vo.
... 0; Mismatches
                       'organism="Bos taurus"
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/mol_type="mRNA"
/db_xref="taxon:9913"
                                            /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
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Plate: 100 row: J column: 1
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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/lab_host="DH108"
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Best Local Similarity 100.C
Matches 39, Conservative
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Best Local Similarity
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BG690967
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                                                                                                     Email: tade@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
V0.5809044.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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Bd19, 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8416
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sall; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease
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Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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                     USDA, ARS, Beltsville Agricultural Research Center Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA Tel: 301 504 8416 Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.0%; Score 39; DB 2; Length 130; 100.0%; Pred. No. 0.0039; ive 0; Mismatches 0; Indels
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252603 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_lib="BARC 5BOV"
                                                                                                                                                                                                                   FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 129 row: G column: 9
Seg primer: ATTAGGTGACACTATAG.
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Flate: 109 row: M column: 24
Seq primer: ATTTAGGTGACATARG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="pooled"
/lab_host="DH108"
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Contact: Sonstegard TS
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39; Conservative
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Bos taurus
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Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."
                                                                                                                                                          Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index Mamm. Genome 13 (7), 373-379 (2002) 22135956
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Sonategard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
Analysis of bovine mammary gland EST and functional annotation of
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos
                                                                                  1 (bases 1 to 134)
Sonsteagard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Comnor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 134;
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                                                                                                                                                                                                                                                                                                USDA, ARS, Beltgville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
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USDA, ARS, Beltsville Agricultural Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
22135956
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/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
/clone_lib="BARC_5BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTACGACG
Blate: 128 row: K column: 1
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9913"
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BE487072
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                                                                                     REFERENCE
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USDA, ARS, Belteville Agricultural Research Center
BB19: 200 Rm 2A, Belteville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: ta6s@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol type="mmNa"
/db xref="taxon:9913"
/tissue_type="mooled"
/lab host="DHIOB"
/clone_lib="BARC 5BOV"
/clone_lib="BARC 5BOV"
/clone_lib="Recror: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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                                                                                                                                                                                           EST 27-MAR-2003
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Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Sonnor, E.B., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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163981 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
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BE486475.1 GI:9606008
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Mismatches
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/organism="Bos taurus"
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BACKWARD: GTTTTCCAGTCACGACG
Plate: 140 row: K column: 13
Seq primer: ATTTAGGTGACATATAG.
Location/Qualifiers
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Best Local Similarity 100.0
Conservative
39; Conservative
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Bos taurus (cow)
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22135956
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BE479391
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BE486475
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VERSION
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Gaps .; 0

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EST 27-MAR-2003

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Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
USDA, ARS, Beltsville Agricultural Research Center
USDA, ARS, Beltsville, MD 20705, USA
Tel: 301 504 8414
Email: tade@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMETS TYCCAGTACACCAT
BACKMARD: GTTTTCCAGTCAGCACG
PLACE: I row: A column: 13
Seq primer: ATTTAGGTGACACTATGG.
Location/Qualifiers
    Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Fax: 301 504 Fax: 301 504
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Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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1 (bases 1 to 142)

2 Sosnesgard, T., Capuco, A.V., White, J., Van Tassell, C.P., Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D., and Quackenbush, J.
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160364 BARC 5BOV Bos taurus CDNA 5', mRNA sequence.
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8416
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/tissue type="pooled"
/lab_host="DH10B"

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    /organism="Bos taurus"

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Best Local Similarity 100.
Matches 39; Conservative
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KEYWORDS
SOURCE
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AUTHORS
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library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
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                                                                                                                                                                                                                                                                                                                                             33 ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT
                                                                                                                                                                                                                                      Query Match 78.0%; Score 39; DB 2; I Best Local Similarity 100.0%; Pred. No. 0.0039; Matches 39; Conservative 0; Mismatches 0;
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Search completed: October 1, 2005, 15:37:40 Job time : 2321.8 secs

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MOLECULE TYPE: c
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                                                       October 1, 2005, 13:15:56; Search time 88.4956 Seconds (without alignments) 924.496 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                      1 atgaaacttctcatccttac......gctgttgctgccaggttaac 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                        1202784 segs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
                                      - nucleic search, using sw model
                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                          Issued Patents NA:*
                                                                                                                                                                                                                 Minimum DB seq length: 0
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Match Length DB
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
ZIP: 94105
ZIP: 94105
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BAR PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/461,333
TI,ING DATE: 05-JUN-1995
TI,ING DATE: 05-JUN-1995
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NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCET DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEPHONE: 415-543-9600
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
INPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR PEDELICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION NUMBER: US 07/619,131
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION NUMBER: US 07/644,745
FILING DATE: 01-DEC-1989
ATTORNEY AGENT INFORMATION:
NAME: Liebescheutz, Joe 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: 1..2
; OTHER INFORMATION: /note= "Overhang"
US-08-154-019-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 37, Application US/08461333 Patent No. 5741957 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA
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CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco CITY: San Francisco CUNTRY: USA

STATE: California COUNTRY: USA

ZIP: 94105

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LOCATION: 64..108
OTHER INFORMATION: /note= "bovine alpha-s1-casein signal
OTHER INFORMATION: peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.0%; Score 39; DB 4; Length 1123; ilarity 100.0%; Pred. No. 7.1e-06; Conservative 0; Mismatches 0; Indels
   LOCATION: 1..1123
OTHER INFORMATION: /note= "bovine alpha-s1-casein mRNA"
                                                                                                                                                                                                                          FEATURE:
NAME/KEY: mat_peptide
LOCATION: 109..705
OTHER INFORMATION: /note= "bovine alpha-s1-casein"
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APPLICATION NUMBER: US/08/153-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,019
FLING DATE: 16-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,333
FILING DATE: 15-JUN-1995
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "bovine alpha-s1-casein
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APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37, Application US/08154019
Patent No. 5633076
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS

LOCATION: 64..708

OTHER INFORMATION: /note= "bo
 OTHER INFORMATION: precursor"
US-08-545-573A-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 39; Conserv
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Gaps

Gaps

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Length 51; Indels

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APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Heyneker, Herbert L.
APPLICANT: Heyneker, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Proper, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
CONDECTIVE OF SECTION OF TRANSPORTION OF TRANSPORTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT
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71.6%; Score 35.8; DB 3;
Best Local Similarity 94.9%; Pred. No. 5.2e-05;
Matches 37; Conservative 0; Mismatches 2;
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REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..2

CTHER INFORMATION: /note= "Overhang"

US-08-464-167-37
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APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-UON-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,798
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37, Application US/09158313
Patent No. 6066725
                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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US-09-158-313-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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APPLICANT: Ritimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,167
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
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                         REFERENCE/DOCKET NUMBER: 16994-003123;
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-543-9600
TELEFAX: 415-543-5043;
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
LENGTH: 51 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..2

COTHER INFORMATION: /note= "Overhang"
US-08-461-333-37
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Patent No. 6013857
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Heyneker, Herbert L.
Platenburg, Gerald
Lee, Sang He
REGISTRATION NUMBER: 37,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deboer, Herman A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Deboer
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 2153, Application US/09949016

Sequence 2253, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307

CURRENT PELLING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 2353
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                                                                                                                                                                                                                                                                                                                                  Query Match
71.6%; Score 35.8; DB 3;
Best Local Similarity 94.9%; Pred. No. 5.2e-05;
Matches 37; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 1..2
OTHER INFORMATION: /note= "Overhang"
         TELERAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
TYPE: nucleic acid
STRANEDNESS: double
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 89.7
Matches 35; Conservative
                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
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US-09-976-594-895
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                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                     Score 35.8; DB 3; Length 51;
Pred. No. 5.2e-05;
0; Mismatches 2; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,798
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US 08/077,788
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION NUMBER: US 07/414,745
FILING DATE: 01-DEC-1989
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 15994-003125
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 ATGAAACTTCTTATCCTCACCTGTCTTGTGGCTGTTGCT
                                                                                                                                                                                                                                            NAME/KEY: misc_feature;
COGATION: 1..2
OTHER INFORMATION: /note= "Overhang"
US-09-158-313-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37, Application US/08476798 Patent No. 6140552 GENERAL INFORMATION:
                TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          Query Match 71.6%;
Best Local Similarity 94.9%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA
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Gaps

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ATTORNEY/AGENT INFORMATION:
NAME: Sweigert PhD, Susan E
REGISTRATION UNDBER: 36,289
REFRENCE/DOCKET UNMBER: 2549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 8015321922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 8015319168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: CHANGE, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT ELLING DATE: 2000-04-14 75
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/231,768
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-00-08
FRIOR FILING DATE: 2000-00-08
FRIOR FILING DATE: 2000-00-08
FRIOR FILING DATE: 2000-00-08
NUMBER: OF SEQ ID NOS: 207012
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Patent No. 5856178
GENERAL INFORMATION:
APPLICANT: White PhD, Kenneth
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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89.7%; Pred. No. 0.0065;
tive 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                   Score 32.6; DB 4; Length 990;
Pred. No. 0.0025;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                    1 ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT 39
                                                                               FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 998930.1.
NAME/KEY: unsure
LOCATION: 984
US-09-976-594-895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14095, Application US/09949016; Patent No. 6812339; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B: Trask Britt and Rossa
P.O. Box 2550
                                                                                                                                                                                                                                                     65.2%;
89.7%;
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 89.7'
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.7'
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salt Lake City
                                       TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-949-016-14095
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US-08-723-306-12/c
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LENGTH: 19480
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SEQ ID NO 895
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regulatory region including
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GENERAL INFORMATION:
APPLICANT: White PhD, Kenneth
APPLICANT: Morrey PhD, John
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Trask Britt and Rossa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,306
FILING DATE:
CLASSIFICATION: 80
ATTORNEY/AGRYT INFORMATION:
NAME: Sweigert PhD, Susan E
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other nucleic acid
/desc = "Downstream primer for Bos
taurus alpha-S1-casein 5' regulato
restriction site linker"
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10041
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STREET: P.O. Box 2550
CITY: Salt Lake City
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                            TELEPHONE: 8015321922
TELEFAX: 8015319168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER.ESTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: other nuc
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Best Local Similarity 97.1
Matches 33; Conservative
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CLASSIFICATION:
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DESCRIPTION:
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38 TCATCCTTACCTGTCTTGTGGCTGTTGC 11
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 28; Conserv
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/desc = "Downstream primer for Capra
hircus beta lactoglobulin 5' promoter region including
restriction site linker"
                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Downstream primer for Bos
DESCRIPTION: taurus alpha-61-casein 5' regulatory region including
DESCRIPTION: restriction site linker"
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08723306
; Sequence 16, Application US/08723306
; Patent No. 5556178
; GENERAL INFORMATION:
    APPLICANT: White PhD, Kenneth
    APPLICANT: White PhD, John
    APPLICANT: Reed, William
    TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
    TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
    VUMBER OF SEQUENCES: 32
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Trask Britt and Rossa
    STREET: P.O. Box 2550
    CITY: Salt Lake City
    STATE: Utah
    CONNTRY: USA
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ZIP: 84110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,306
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CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweigert Phb, Susan E
RECISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 38 base pairs TYPE: nucleic acid
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TOPOLOGY: not relevant
MOLECULE TYPE: other nuc
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Best Local Similarity 100.
Matches 28; Conservative
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39 base pairs
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Best Local Similarity
Matches 33; Conserv
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DESCRIPTION:
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TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
TYPE: not relevant
DESCRIPTION: /desc = "Downstream primer for Capra
DESCRIPTION: hircus beta lactoglobulin 5' promoter region including
PDESCRIPTION: restriction site linker"
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                                                                     APPLICANT: White PhD, Kenneth
APPLICANT: White PhD, John
APPLICANT: Morrey PhD, John
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Trask Britt and Rossa
STREET: P.O. Box 2550
CITY: Salt Lake City
STATE: Utah
COUNTRY: USA
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Patent No. 6528699
GENERAL INFORMATION:
TITLE OF INVENTION: TRANSGENICALLY PRODUCED
TITLE OF INVENTION: TRANSGENICALLY PRODUCED
TITLE OF INVENTION: NON-SECRETED PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 TCATCCTTACCTGTCTTGTGGCTGTTGC 38
PCT-US96-10041-16/c
; Sequence 16, Application PC/TUS9610041
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sweigert PhD, Susan E
REGISTRATION NUMBER: 36,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 8015321922
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INFORMATION FOR SEQ ID NO: 16:
SEGUIENCE CHARACTERISTICS:
LENGTH: 38 base pairs
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11 TCATCCTTACCTGTCTTGTGGCTGTTGC 38

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Sequence 12853, A
Sequence 953, App
Sequence 10691, A
Sequence 9038, Ap
Sequence 14946, A
Sequence 5742, Ap
Sequence 14242, Ap
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(cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

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(cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-960-352-963
US-09-960-352-10691
US-09-960-352-1946
US-09-960-352-14946
US-09-960-352-14242
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                             Copyright
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c 11	39	78.0	417	σ	US-09-960-352-13070	~	3070, A
	39	78.0	428	σ	US-09-960-352-4083	Sequence 4(383, Ap
13	39	78.0	428	σ	US-09-960-352-13294	Sequence 1	3294, A
	39	78.0	432	6	US-09-960-352-304	Sequence 3	04, App
c 15	39	78.0	434	σ	US-09-960-352-12097	Sequence 1	2097, A
16	39	78.0	435	σ	US-09-960-352-1668	Sequence 1	568, Ap
	39	78.0	437	σ	US-09-960-352-14237	Sequence 1	14237, A
	39	78.0	440	6	US-09-960-352-741	Seguence 7	41, App
c 19	39	78.0	445	σ	US-09-960-352-11394	Sequence 1	
50	39	78.0	450	6	US-09-960-352-712	Sequence 7	12, App
21	39	78.0	1123	8	US-08-545-573A-40	Sequence 4	0, Appl
22		74.8	89	13	US-10-079-623-333	Sequence	
23		74.8	384	σ	US-09-960-352-4568	Sequence 4	
		74.8	413	Φ	US-09-960-352-9483	Sednence 9	9483, Ap
c 25	37.4	74.8	417	σ	US-09-960-352-1673	Seguence 1	673, Ap
	7.	74.8	420	σ	US-09-960-352-761	Sequence 7	61, App
	7	74.8	443	σ	US-09-960-352-14939	Sequence 1	4939, A
28	δ.	71.6	51	16	US-10-170-221-37	Sequence	37, Appl
29	'n.	71.6	21	22	US-10-987-587-37	Seguence	37, Appl
c 30	ď	9.59	471	σ	US-09-960-352-5980	Sequence 5	980, Ap
31	32.6	65.2	268	σ	US-09-960-352-1901	Sequence 1	1901, Ap
32	ď.	65.2	415	σ	US-09-960-352-8818	Seguence 80	318, Ap
33	ď	65.2	981	21	US-10-956-157-723	Seguence	723, App
34	ď	65.2	981	51	US-10-956-157-5958	equence	5958, Ap
35	ä	62.8	82	13	US-10-079-623-113	equence	113, App
36	31	62.0	349	σ	US-09-960-352-2374		2374, Ap
37	31	62.0	668	σ	US-09-897-006-12	Sequence 1	
38	31	62.0	699	10	897-511A-	Φ	
33	31	62.0	668	17	-10-397-079-1	equence	'n
40	31	62.0	668	20	US-10-759-315-12	ø	à
41	31	62.0	668	21	-10-947-881-1	equence	'n
42	31	62.0	668	23	1-018-895-1	edneuce	
43	30	0.09	588	24	-11-097-143-3	edneuce	ä
44	29	58.0	93	13	9-623-29	Sequence	ď
45	27.8	55.6	752	17	-10-085-198-4	Sequence	٠.
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					ALIGNMENTS		

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RESULT 1

US-09-60-352-12853/C

US-09-60-352-12853, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Tao, Neabley C.

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: MUCLEIC AND PAT DEPOSITION

TITLE OF INVENTION: MUCLEIC AND PAT DEPOSITION

CURRENT PELLING DATE: 2010-09-24

CURRENT PELLING DATE: 2010-09-24

SEQ ID NO 12853

LENGTH: 337

TYPE: DNA

ORGANISM: Bos taurus

FATURE:

FATURE:

FATURE:

CORATION: (32)

OTHER INFORMATION: Unsure at all n locations

OTHER INFORMATION: Clone ID: 55-LIB2809-027-Q1-E1-F4

US-09-960-352-12853

Query Match

Best Local Similarity 100.0%; Pred: No. 3.3e-05;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Sequence 14946, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 14946
LENGTH: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: WUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: WOSCIE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 408
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 39-LIB2809-013-Q1-E1-B12
US-09-960-352-9038
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) OTHER INFORMATION: Clone ID: 64-LIB2809-027-Q1-E1-H8
US-09-960-352-14946
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Pred. No. 3.4e-05;
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100.0%; Pred. No. ...
0; Mismatches
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Patent No. US20020137139A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 39; Conservative
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                                                                                                                                                                                                                                                    LENGTH: 394
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                                                                                                                                                      Sequence 953, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Warren, Wealey C.
APPLICANT: Tao, Nengbing
APPLICANT: Byati, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILLE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT PILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 375
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Sequence 10691, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: WISCLE AND FAT DEPOSITION
FILLE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 10691
LENGTH: 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.0%; Score 39; DB 9; Length 375; 100.0%; Pred. No. 3.4e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 46-LIB2809-027-Q1-E1-D6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAAACTICTCAICCTTACCTGTCTTGTGGCTGTTGCT 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 05-LIB188-007-Q1-E1-B9
                            ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT
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Patent No. US20020137139A1
GENERAL INFRMATION:
APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 39; Conservative
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US-09-960-352-9038/c
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Sequence 4541, Application US/09960352

Sequence 4541, Application US/09960352

Sequence 4541, Application US/09960352

SEQUENCE IN O. US2002013713941

SEQUENCE IN O. US2002013713941

APPLICANT: Warren, Wesley C.

APPLICANT: Byact, John C.

APPLICANT: Byact, John C.

APPLICANT: Byact, John C.

APPLICANT: Mathialgan, Nagappan

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006.37-21(10298) C.

CURRENT FILING DATE: 2001-09-24

SEQ ID NOS: 15112

SEQ ID NO 4541

LENGTH: 413
                                                                                                                Sequence 12666, Application US/09960352
Patent No. US2002013713941
GENERAL INFORMATION:
APPLICANT: Tao, Neaglay C.
APPLICANT: Tao, Neaglay C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
APPLICANT: MATHIALORY NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
NUMBER OF SEQ ID NOS: 15112
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253 ATGAAACTICTCATCCTTACCTGTCTTGTGGCTGTTGCT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 54-LIB2809-027-Q1-E1-F6
US-09-960-352-12606
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; OTHER INFORMATION: Clone ID: 20-LIB2809-001-Q1-E1-E7
US-09-960-352-4541
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Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.4e-05;
iive 0; Mismatches 0;
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 39; Conservative
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US-09-960-352-4541/c
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LENGTH: 412
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Patent No. US20020137139A1

GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, MacLeIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 14242
LENGTH: 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Wasley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nongapan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLELE AND FAT DEPOSITION
FILE REPERENCE: 16511.066/37-21 (10289)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 9712
LENGTH: 411
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                                                                                                                           Query Match 78.0%; Score 39; DB 9; Length 408; Best Local Similarity 100.0%; Pred. No. 3.4e-05; Matches 39; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.0%; Score 39; DB 9; Length 408; 100.0%; Pred. No. 3.4e-05;
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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 61-LIB2809-013-Q1-E1-H10
US-09-960-352-14242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 Argaactrerearcerracererererereseristee 289
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; OTHER INFORMATION: Clone ID: 42-LIB2809-010-Q1-E1-C6
US-09-960-352-9712
                          ) ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 25-LIB2809-002-Q1-E1-G1
US-09-960-352-5742
                                                                                                                                                                                                                              1 ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT 39
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Matches 39; Conservative
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Matches 39; Conserv
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCA AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 304
LENGTH: 432
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APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: WOSCLE AND FAT DEPOSITION
TITLE OF INVENTION: WOSCLE 16511.0066/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 12097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Bos taurus
) OTHER INFORMATION: Clone ID: 02-LIB2809-032-Q1-E1-A5
US-09-960-352-304
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; OTHER INFORMATION: Clone ID: 52-LIB188-014-Q1-E1-E12
US-09-960-352-12097
       OTHER INFORMATION: Clone ID: 57-LIB2809-005-Q1-E1-G2
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5. 3.4e-05;
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                                                                                                                 78.0%; Score 39; DB 9; L
100.0%; Pred. No. 3.4e-05;
ive 0; Mismatches 0;
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3.4e-05;
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Patent No. US20020137139A1
GENERAL INFORMATION:
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Patent No. US20020137139A1
GENERAL INFORMATION:
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Best Local Similarity 100.(
Matches 39; Conservative
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Best Local Similarity
Matches 39; Conserv
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                  , OTHER ANTONIO
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| Sequence 1082002013713941
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| APPLICANT: Tao, Nengbing |
| APPLICANT: Tao, Nengbing |
| APPLICANT: Tao, Nengbing |
| APPLICANT: Mathialagan, Nagapan |
| TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND |
| TITLE OF INVENTION: MUSELE AND FAT DEPOSITION |
| TITLE OF INVENTION: MUSER: US/09/960,352 |
| CURRENT FILING DATE: 2001-09-24 |
| SEQ ID NOS: 15112 |
| SEQ ID NOS: 15112 |
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Patent No. US2002013713941
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Warren, Wealey C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 13112
LENGTH: 428
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEE ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298) C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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Pred. No. 3.4e-05;
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                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 56-LIB2809-013-Q1-E1-F8
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ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 18-LIB2809-024-Q1-E1-E5
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100.0%; Pred. No. ...
0; Mismatches
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Matches 39; Conservative
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Matches 39; Conserv
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                                                                                                                                                                                                                                                         SEQ ID NO 13070
LENGTH: 417
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Search completed: October 1, 2005, 15:58:56 Job time : 466.372 secs

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